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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX167589
BC014825
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AB004267
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AF181984
AB023027
AX166520
AB021864
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AX399682
BC032787
AF428261
AK095713
BC021840
AF428262
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CBRG46J06
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BC017634
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AX167585
AF286366
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-MODEL=frame+_p2n.model.-DEV=Xlh
-Q=/Cgn2_1/GSPTO_spool/US09960643/runat_07032003_090517_19877/app_query.fasta_1.647
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-UNITS=btits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-OUTPWT=pto -NORM=ext -HBAPSIZE=500 -MINLEN-0 -MAXLEN=2000000000
-USER=US09960643_@CGN_1_1_2496_@runat_07032003_090517_19877 -NCPU=6 -ICPU=3
-NO_XLEXY -NO_MANAP -LARGEORERY -NGC_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                 (without alignments) 3239.695 Million cell updates/sec
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                                                                                                                           March 15, 2003, 05:00:47; Search time 4276 Seconds
               GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                     nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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AL049688 Human gen AX399682 Sequence BC032787 Homo sapi AK095713 Homo sapi BC0121840 Mus muscu BG557 Ratus norv AX16517 Sequence AX16517 Sequence AX16517 Sequence AX16518 Sequence AX16518 Sequence BC014825 Mus muscu L2288 Rattus norv AM04267 Rattus norv AM04267 Rattus norv AX1819102 Sequence AX29863 Sequence BC001921 Homo sapi BC001926 Homo sapi BC001926 Homo sapi BC017363 Homo sapi BC017363 Homo sapi BC017363 Homo sapi

ALIGNMENTS

X58995 Mouse mRNA S65840 Ca2+/calmod M64757 Rat Ca++/ca

AL365314 Mouse DNA AC022675 Mus muscu M64176 D.discoideu

Rattus norv

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OLVSGGELFDFILERGVYFETDASLVLOUSAVKYLHENGIVHRDLKPENLLYLTPE
ENSKIMITDFGLSKWERDNGINSTACOTPGYVAPEVLAQKPYSKAVDCWSIGVITYILL
CGYPPFYEETESKLEKIKGGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKA
LENPWINGANTALHRDIYPSYSLOIGNERAKSKWRAQANAAAVHHMRKLHANNLHSPGV
RPEVENRPPETGYSTSRPSSPEITITTEAPVLDHSYALDAITOLPOCHGRRPTABGSF
SLNCLVNGSLHISSSLVPMHQGSLAAGPCGCCSSCLNIGSKGKSSYCSEPTLLKKANK
             HS272L161 1738 bp mRNA linear PRI 21-APR-1999 Human gene isolated from PAC 272L16, chromosome 1, similar to calcium/calmodulin dependent protein kinases.
                                                                                                                                                                                                                                      at
                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1738)
                                                                                                                                                                             Submitted (21-APR-1999) E-mail contact: humquery@sanger.ac.uk Submitted (21-APR-1999) E-mail contact: humquery@sanger.ac.uk rhis sequence was generated from CDNA clones isolated using sequence from the bacterial clone 272116 (AL023764) and EST data. The EST sequences listed match this sequence with an identity of a least 95% between the coordinates shown.

Further information can be found at http://www.sanger.ac.uk/HGSP/Chrl/ Partial, experimentally determined gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="matches EST AI215131 from clone IMAGE:1925595"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            // (1469. 1550,1553. .1723,1721. .1738)
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Location/Qualifiers
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651
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108. 236
/number=2
237. 311
/number=3
312. 450
/number=4
/number=5
/number=5
/number=5
/number=5
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                                                                                                 Homo sapiens.
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              LOCUS
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TITLE
JOURNAL
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140
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                                                                                                                                                                                                                                                                                                               GlyThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLysAlaVal
                                                                                               LysThrPhellePheMetGluValLeuGlySerGlyAlaPheSerGluValPheLeuVal
                                                                                                                                                                  ValThrLeuGluAspIleTyrGluSerThrThrHisTyrTyrLeuValMetGlnLeuVal
                     1738
476
0
0
0
                           Matches:
Conservative:
Mismatches:
357
                                             Indels:
                       Length:
                                                   Gaps:
                                                              US-09-960-643-2 (1-476) x HS272L161 (1-1738)
 9
458
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Alignment Scores: Srore: Fercent Similarity: Query Match: DB:	US-09-960-643-2 (1-476) QY 1 MetGlyArgLySGl	Db 70 ATGGGTGGAAAGGA Qy 21 LysThrPheilePh	Db 130 AAAACCTTCATTTT OY 41 LysGlnArgleuTh	Db 190 AAGCAAAGACTGAC Qy 61 ArgAspSerSerLe	Db 250 CGGACAGCGCCT Oy 81 VAIThrieuGluAs	Db 310 GTGACCCTGGAGGA OY 101 SerGlyGlyGluLe	Db 370 TCTGGTGGGAGCT Oy 121 SerieuValileG1	Db 430 AGTCTGGTGATCCA OY 141 HisargaspleuLy	Db 490 CACAGAGACTTAAA Ov 161 MetileThraspPh	550	Qy 181 GlyThrProGlyTy 	201	670	Qy 221 GluGluThrGluSe 	241	Db 790 CCATTCTGGGATGA	850	Qy 281 ThralaLeuHisAr 	Qy 301 LysSerLysTrpAr
LysSerLysTrpArgGlnAlaPheAsnAlaAlaAlaValValHisHisMetArgLysLeu 320	GinalaSerGluthrSerargProSerSerProGluIleThrIleThrGlualaProVal 360 	LeuAspHisSerValAlaLeuProAlaLeuThrGlnLeuProCysGlnHisGlyArgarg 380 	ProthralaProGlyGlyArgSerLeuAsnCysLeuValAsnGlySerLeuHisIleSer 400 	SerSerLeuValProMetHisGlnGlySerLeuAlaAlaGlyProCysGlyCysCysSer 420	SerCysLeuAsnIleGlySerLysGlyLysSerSerTyrCysSerGluProThrLeuLeu 440 	IysLysAlaAsnLysLysGlnAsnPheLysSerGluValMetValProValLysAlaSer 460 	GlySerSerHisCysArgAlaGlyGlnThrGlyValCysLeuIleMet 476	AX399682	AX399682.1 GI:2133545.	human. Homo sapiens Figherwise Charlets Wastahrsts Butalonstomi.	Eukaijota, metazoa, choluata; Mammalia; Eutheria; Primates; I		Location/Qualifiers e 12447	/organism="Homo sapiens" /db_xref="taxon:9606" 701500	/note="unnamed protein product" /codon_start=1 /protein_id="cab33521.1"	/db_xref="G1:2133456" /translation="MGKREPDICSSWKKQTINIRKTFIFMEVLGSGAFSEVFLVKQRL ncklratkCoardnos:TRNTATKFENTVNTRNTVTVCTNNTVSC	AND THE THE CARRY OF THE CONTROLL THE THE THE THE THE THE CARRY OF THE	I DENT LENGE THE STEP OF THE S	590 a
Qy 301 Db 918 Qy 321 Db 978	Qy 341 Db 1038	Qy 361 Db 1098	Qy 381 Db 1158	Qy 401 Db 1218	Qy 421 Db 1278	Qy 441 Db 1338	Qy 461 Db 1398	RESULT 2 AX399682 LOCUS	DEFINITION ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE	TITLE	FEATURES SOURC	CDS					BASE COUNT ORIGIN

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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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UIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Contact: MGC help desk
Contact: MGC help desk
Email: capabb.*Tefmail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@hngfi.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brincley,C.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC032787 27-JUN-2002 Homo sapiens, calcium/calmodulin-dependent protein kinase IG, clone MGC:44894 IMAGE:5179957, mRNA, complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 2474)

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Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                    1330 AGCTGCCTGAACATTGGGAGCAAAGGAAAGTCCTCCTACTGCTCTGAGCCCACACTCCTC 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGACCACAGTGTAGCACTCCCTGCCCTGACCCAATTACCCTGCCAGCATGGCCGCGGG 1209
                                                                                                                                                                                                       LeuAspHisSerValAlaLeuProAlaLeuThrGlnLeuProCysGlnHisGlyArgArg 380
                                                                                                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 SerCysLeuAsnIleGlySerLysGlyLysSerSerTyrCysSerGluProThrLeuLeu 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysLysAlaAsnLysLysGlnAsnPheLysSerGluValMetValProValLysAlaSer 460
  HisMetAsnLeuHisSerProGlyValArgProGluValGluAsnArgProProGluThr
                                                                                                    GlnAlaSerGluThrSerArgProSerSerProGluIleThrIleThrGluAlaProVal
                                                                                                                                                                                                                                                                                                                                                                                                           SerSerLeuValProMetHisGlnGlySerLeuAlaAlaGlyProCysGlyCysCysSer
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Clone distribution: MGC clone distribution information can be found

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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 68 Row: k Column: 17
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gl: 14196444.
Location/Qualifiers
                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="LocusID:57172"
/db_xref="Laxon:9606"
/db_xref="taxon:9606"
/clone="MGC:44894 IMAGE:5179957"
/tissue_type="Brain, Lung, Testis, adult, pooled whole"
/clone_lib="NHH MGC_115"
/lab_host="DH108"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249
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EMRB,

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 2464)
Schutte, B.C., Bjork, B.C., Coppage, K.B., Malik, M.I., Gregory, S.G., Schutte, B.C., Bjork, B.C., Watanabe, Y., Dixon, M.J. and Murray, J.C.
A preliminary gene map for the Van der Woude syndrome critical Genome Res. 10 (1), 81-94 (2000)
                                                                                                                        I gamma
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                                                                                                                                                                             Genetics, University of Iowa, 140
                                                                                                                        Kinase
                                                                                                  Chases 1 to 2464)
Bjork, B.C., Watanabe, Y., Murray, J.C. and Schutte, B.C.
Characterization of the human ortholog of rat CaM Kin
(CamKIG) at 1g32-q41
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Blork, BC., Watanabe, Y., Murray, J.C. and subjork, BC., Watanabe, Y., Murray, J.C. and submitted (05-0CT-2001) Genetics, University, IA 52242, USA
Lowa City, IA 52242, USA
Lowacity, 12 52464
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Conservative:
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/gene="CAMK1G"
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                                               AspProAsnGluArgTyrThrCysGluLysAlaLeuSerHisProTrpIleAspGlyAsn
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                   ATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGGCATCATGTCCACTGCCTGT
                                    GlyThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLysAlaVal
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                                                               HisArgAspLeuLysProGluAsnLeuLeuTyrLeuThrProGluGluAsnSerLysIle 160
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Homo sapiens cDNA FLJ38394 fis, clone FEBRA2007534, moderately similar to CamKI-like protein kinase. AK095713 AK095713 Olion camking a AK095713. GI:21755035
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Isogal, T. and Yamanoto, J.

Direct Submitssion

Submitted (04-JU1-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7

Razusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

Razusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mall:genomics@hri.co.jp, Tel:81-438-52-3986)

REDO human CDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB) ilbrary

Construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugiyama, T. Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishi, S., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishi, S., Yamannoto, J., Isono, Y., Kawal-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K., and Isogai, T., Nebo, human, CDNA, sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                    1393 AAAAAGGCCAACAAAAAACAGAACTTCAAGTCGGAGGTCATGGTACCAGTTAAAGCCAGT 1452
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Homo sapiens fetal brain cDNA to mRNA, clone_lib:FEBRA2
clone:FEBRA2007534.
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/clone="FEBRA2007534"
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/clone_lib="FEBRA2"
/dev_stage="fetal"
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99ThrPheilePheMetGluValLeuGlySerGlyAlaPheSerGluValPheLeuVa 111111111111111111111111111111111111	GGACAGCAGCAGAATGCATTGCTTGAAAAAGATCAGCATGAAAACAT ThrLeuGluAspIleTyrGluSerThrThrHisTyrTyrLeuValMetGlnLeuVa [IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		MetileThraspPheGlyLeuSerLysMetGluGlnAsnGlyIleMetSerThralaCys	ASPCYSTTpSerlleGlyVallleThrTyrlleLeuLeuCysGlyTyrProProPheTyr 	ProPhefrpAspAspIleSerGluSerAlaLysAspPhefleCysHisLeuLeuGluLys	ThralaLeuHisargaspIleTyrProSerValSerLeuGlnIleGlnLysasnPheala	HisMetAsnLeuHisSerProGlyValArgProGluValGluAsnArgProbroGluThr
21 306 41 366 61	426 81 486 101	546 121 606 141 666	161 726 181 786	201 846 221 906	241 966 261 1026	281 1086 301 1146	321 1206 341 1266 361 1326
cy Cy Cy	Db Qy Db	90 00 00 00 00 00 00 00 00 00 00 00 00 0	9y 0y 0b	0y 0y 0b	o da da da	o o o o	

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Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 41 Row: i Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                                                                                                                                                                                                  BC021840 2416 bp mRNA linear ROD 07-AUG-2002 Mus musculus, clone MGC:30513 IMAGE:4502479, mRNA, complete cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 2416)
Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (18-2AN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.
Richards, S., Gibbs, R.A.
1566 AAAAAGGCCAACAAAAAAACAGCAACTTCAAGTCGGAGGTCATGGTACCAGTTAAAAGCCAGT 1625
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Contact: MGC help desk
Contact: MGC help desk
Contact: MGC help desk
Contact: MGC help desk
Tissue procurement: The Cepko Laboratory
Tissue procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BGN-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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/clone_lib="NIH_MGC_94"
/lab_host="DH10B"
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/translation="MGRKEEEDCSSWKKQTTNIRKTFIFWEVLGSGAFSEVFLVKQRV
TGRLFALKCTKSPAREDSSSLENEIATURINTHENTYLEDITSETTHYLVMQLVSG
GELPDRILEGGYTTRECASLVIGOVLSAVKYLHENGITVHRDLKPERLLYTLPPEENSKI
MITDFGLSKMEONGVWSTACGTPGYVAPEVLAOKPYSKAVDCWSIGVITYILLCGYPP
TSPETESKLFERKIRGOYTEFESPFWDDISESARDFIGHLLERDPDRETYTCERALRHPW
IDGNTALHRDITVPSYGLOGNNGARANTHAKKLHMMLHSFSYNGEYE
NRPPVSPAPEVSRPDSHDSSITEAPILDPSTPLPALTRLPCSHSSRPSAPSGGRSLNC
KINGSLRISSSLVPMQQGPLATGPCGCCSSCLNIGNKGKSSYCSEPTLFRKANKKONF
KSPWYNPVKAGGTYCVLW"

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Conservative:
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Bjork, B.C., Watanabe, Y., Murray, J.C. and Schutte, B.C. Characterization of the human ortholog of rat CaM Kina (CaMKrg) at 1q32-q41
Unpublished
2 (bases 1 to 2427)
Bjork, B.C., Watanabe, Y., Murray, J.C. and Schutte, B.C. Direct Submission
Submitted (O5-COT-2001) Genetics, University of Iowa, Iowa City, IA 52242, USA
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Sciurognathi; Muridae;
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7. Grganism="Mus musculus"
Ab_xref="taxon:10090"
/chromosome="1"
/map="1H, 104.00 cM"
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Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
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Yokokura, H., Terada, O., Naito, Y. and Hidaka, H.
Isolation and comparison of rat cDNAs encoding
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or Protein Kinase,
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Rattus norvegicus embryo (E18)
Nakanishi clone:NS.
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
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D86557
D86557.1 GI:2077933
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//protein_id="AAL28101.1"
//Lanslation="ROTEST94"
//translation="ROTEST94"
//translation="ROTEST94"
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MITDRGLSKMEQNYRATRAGTPESVYAPEVLAQKPYSKAVDCWSIGVITYILLGGYPP
FYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLENDPNERYTCEKALRHP
                                                                                                                                                                                            IDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNLHSPSVRQEVE
NRPPVSPAPEVSRPDSHDSSITEAPILDPSTPLPALTRLPCSHSSRPSAPSGGRSLNC
LVNGSLRISSSLVPWQQGPLATGPCGCCSSCLNIGNKGKSSYCSEPTLFRKANKKQNF
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| AAGCAAAGAGTGACTGGGAAACTCTTTGCTCTGAAATGTATCAAGAAGTCACCAGCCTTC
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Matches:
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Mismatches:
Indels:
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694 c 601 g 547 t
                       /note="corresponds to EST
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94.97%
92.03%
92.62%
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07-FEB-1999

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 107).
Plowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R., Flanagan, P. and Clary, D.S.
Novel human protein kinases and protein kinase-like enzymes
Patent: WO 0138503-A 8 31-MAY-2001;
Sugen, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                PAT 22-JUN-2001
                                                                                                                                                                                                                                                                                        ProPheTrpAspAspIleSerGluSerAlaLysAspPheIleCysHisLeuLeuGluLys 260
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258 c 276 g 22:
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Sequence 8 from Patent WO0138503
AX166517
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Submitted (15-JUL-1996) Hisayuki Yokokura, Nagoya University School
of Medicine, Department of Pharmacology; Tsurumai 65, Showa-ku,
Nagoya, Aichi 466, Japan (Tel:052-744-2075, Fax:052-744-2083)
Location/Qualifiers
                                                                                                                                                                                              /note="similar to calcium/calmodulin-dependent protein
kinase I mmAA (L24907, L26288)"
/codon_start=1
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Biochim. Biophys. Acta 1338 (1), 8-12 (1997)
97228532
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Matches:
Conservative:
Mismatches:
Indels:
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'Organism="Rattus norvegicus"

/db_xref="taxon:10116"

/clone="N5"

/rissue_type="brain"

/clone_lib="S. Nakanishi"

/dev_stage="embryo (E18)"
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1612.00
99.68%
98.38%
64.15%
                                     2 (bases 1 to 1013)
Yokokura, H.
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Best Local Similarity:
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                  JOURNAL
MEDLINE
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/db_xref="taxon:9606"
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                                       Location/Qualifiers
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                                                                             ValSerGlyGlyGluLeuPheAspArgIleLeuGluArgGlyValTyrThrGluLysAsp
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(Loases 1 to 1074)
Donobio,G., Scoville,J., Turner,C.A., Friedrich,G., Zambrowicz,B. Abuin,A. and Sands,A.T.
Novel human kinase proteins and polynucleotides encoding the sampatent: WO 0142435-A 3 14-JUN-2001;
Lexicon Genetics Incorporated (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1158)
Donoho, G., Scoville, J., Turner, C.A., Friedrich, G., Zambrowicz, B., Abuin, A. and Sanda, A.T.
Novel human kinase proteins and polynucleotides encoding the same patent: WO 0142435-A 114-JUN-2001;
Lexicon Genetics Incorporated (US)
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Submitted (11-JUL-2000) Dept. Pulmonary Diseases, University
Medical Center Utrecht, Heidelberglaan 100, Utrecht 3584 CX,
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            AlaSerLeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIle
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 1579)
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Identification and characterization of CKLiK: a 1Ca2+/calmodulin-dependent kinase
Blood (2000) In press
2 (bases 1 to 1579)
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Enkaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1671)

Donoho, G., Scoville, J., Turner, C.A., Friedrich, G., Zambrowicz, B., Abuin, A. and Sands, A.T.

Abuin, A. and Sands, A.T.

Povel human kinase proteins and polynucleotides encoding the same with the model of the same of the same and the same better wo 0.44.435-A 5.14-JUN-2001;

Lexicon Genetics Incorporated (US)
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                  GluLysAspProAsnGluArgTyrThrCysGluLysAlaLeuSerHisProTrpIleAsp
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1 437 c 448 g 333
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Sequence 5 from Patent W00142435.
AX167589 GI:14596988
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//Product="CamKI-like protein kinase"
//Product="CamKI-like protein kinase"
//Product="CamKI-like protein kinase"
//Product="CamKI-like protein kinase"
//Ab_xref="GI:0937341"
//Ab_xref="GI:0
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/db_xref="taxon:9606"
/cell_type="eosinophil"
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γQ	8 0	<pre>11eValThrLeuGluAspIleTyrGluSerThrThrHisTyrTyrLeuValMetGlnLeu 99 11 </pre>	
γq	100	ValSerGlyGlyGluLeuPheAspargIleLeuGluArgGlyValTyrThrGluLysAsp 119 	
ъ д	120	AlaSerLeuvallleGinGlnValLeuSerAlavalLysTyrLeuHisGluAsnGlyIle 139 ::: ::	
ъа	140	ValhisargaspleulysProGluasnleuleuTyrleuThrProGluGluasnSerLys 159 	
y d	160	IleMetIleThraspPheGlyLeuSerLysMetGluGlnasnGlyIleMetSerThr 178 	
<u>ب</u> م	179	alacysglythrproglytyrValalaprogluValleualaginlysprotyrSerlys 198 	
۵ ہ	199 767	AlavalAspCysTrpSerIleGlyvalIleThrTyrIleLeuLeuCysGlyTyrbroPro 218 	
<u>م</u> د	219 827	PheTyrcluGluThrGluSerLysLeuPheGluLysIleLysGluGlyTyrTyrGluPhe 238 ::: :::	
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<u>ک</u> ۵	259	GluLysaspProasnGluargTyrThrCysGluLysalaLeuSerHisProTrpIleasp 278 	
۵ ۸	279	GlyasnThralaLeuHisargAspileTyrProSerValSerLeuGlnIleGlnLysasn 298 :::	
չ d	299	PheAlaLysSerLysTrpArgGlnAlaPheAsnAlaAlaAlaValValHisHisMetArg 318 	
γq	319	LysLeuHisMetAsnLeuHisSerProGlyValArgProGluValGluAsnArg 336 ::: AAACTACACCTCGGCAGCAGCAGGTGTAAATGCAAGTGTTTCGAGCAGCACGTCAGT 1186	
ъ a	337	0 ·· c	
λQ	356 1246	ThrGlualaProValLeuAspHisSerValalaLeuProAla	
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λ.	380	384	
ڡۣ	1425	GAGGACIGITIGAGITCAGGAGITITAAGACCAGCCIGACCAACAIGGIGAAACCCCAIC 1484	

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clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 23 ROW: j Column: 19 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

Location/Qualifiers

1. .1448

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/ tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy."
//lab_host="DH10B"
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kinase I"
/protein.id="AAH14825.1"
/db_xref="GI:15928726"
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Strausberg,R.
Direct Submission
Sounitted (01-00-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X., Hulyk, S.W., Hale, S.M., S., Martin, R.G., Muzny, D.M.,
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                                     1485 TCTACTAAAATATAAAAATTAGCCGGGTGTGGTGGCGGCACCACTGTAATGTCAGCTACTT 1544
                                                                                                       395 GlySerLeuHisIleSerSerSerLeuValProMetHisGlnGlySerLeuAlaAlaGly 414
                                                                                                                                                                                                          415 ProCysGlyCysCysSerSerCysLeuAsnIleGlySerLysGlyLysSerSerTyrCys 434
-----GlyGlyArgSerLeuAsnCysLeuValAsn 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunarathe, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.R.
Richards, S., Gibbs, R.A.
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Mus musculus, Similar to calcium/calmodulin-dependent protein kinase 1, clone MGC:18933 IMAGE:3969343, mRNA, complete cds.
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                                                                                                                               /note="Vector: pCMV-SPORT6"
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SDFGLSKMEDPGSVLSTAGGTPGYVAPENLAGKYSKANDCKSTGVIAT
YDENDAKLFOLIKAEYSETSPYWDDISDSAKDFIRHLMEKDPERRFTCEQALQHPWI
AGDTALDKNIHQSYSEQIKKNPAKSKNKQAFNATAVVHHMRKLQLGFSQEGGGGTASH
GELLTPTAGGPAAGCCCRDCCVEPGSELPAPPPSSRAMD"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                        SerValSerLeuGlnIleGlnLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsn
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Cho,F.S., Phillips,K.S., Bogucki,B. and Weaver,T.E.
Cho,F.S., Phillips,K.S., art cDNA clone encoding
calcium/calmodulin-dependent protein kinase I
Blochim. Blophys. Acta 1224 (1), 156-160 (1994)
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ke protein kinase mRNA,
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L lung cDNA to mR

    1439
    /organism="Rattus norvegicus"

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/db_xref="GI:439614"
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/db_xref="taxon:10116"
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1439 249 : 51 85 90		eMetGluvalLeuG ::: CAGGGATGTTCTGG	3lyLysLeuPhe	CAGAAACTGGTG	rLeuGluAsnGluI	AspileTyrGl	ipAr 	. 8	eGlnGlnValLeuS CTTCCAGGTGCTGG	roGluAsn CAGAGAAC	AspPheGlyLeuSerI 	ValAl 	pSerIleGlyVall 	3luSerLysLeu :::::: SATGCCAAACTT	paspaspileser(SluArgTyrThr ::: :: AAGAGGTTCACC	HisArgaspileTy1 	STrpArgGlnAlaH ::: GTGGAAGCAAGCTT	etAsnLeuHisSerProGl ::
Length: Matches: Conservative: Mismatches: Indels: Gaps:	(1-1439)	LysThrPhellePhe ::: GATATTTATGACTTC	GlnArgLeuThr	CAAGAGGACT	PheArgAspSerSer	Leug]	- G1,	AGGTGG	SpAlaSerLeuVallle 	/alhisargaspLeuLysP 	MetileThr :::	CysGlyThr 	ValAspCysTr 	PheTyrGluGluThrC ::: TCTATGATGAAAATC	luSerProPheTr::!	SluLysaspProas Sagaaagacccaga	pGlyAsnThrAlaLeuk ::: AGGAGACAGCTCTG	ASnPheAlaLysSerLys 	LysLeuHisMetAsr
1.51e-73 1155.50 64.66% 45.98%	x RATCAMPKAA (rThrAsnileArg ::: CAGAAGACATTAGG	luValPheLeuVal	CTGGCA	SLYSSerProAla	PLYSH1SGluAsn	<pre>yrTyrLeuValMetGlnLeuValSe ::: </pre>	rcarcargcagcrg	altyrthrGluLysAspA CTACACAGAACGGGATC	isGluAsnGlyIleValH ::: CGACCTGGGCATTGTGC	GluGluAsnSerLysIle ::: :::	IleMetS :::::: srgcrc	분드의	ysGlyTyrProProPhe 	ryrTyrGluPhe 	IleCysHisLeuLeu(::: ATACGTCATTTGATG	HisProTrp1leAsp(CACCCTGGATTGCA	lnIleGlnLys aGATCAAGAAG	alHisHisMetArg
Scores: : imilarity: l Similarity: ch:	-643-2 (1-476)	TrpLysLysGlnTl TGGAAGCAGGG	lyAlaPhes	GCCTTCT	LysCysIleLys	ceutystys	hrHisTyrTyr 	GCCACCTCTACC	GluargGlyValTy ::: GAGAAAGGATTCTA	VallysTyrLeuHi:	TyrLeuThrProG	luGlnAsnGly AGGACCCAGGC	ValLeuAlaGlnLysF 	TyrIleLeuLeuCys TATATACTGCTCTG1	LyslleLysGluGly' ::: ::: cagaTTTGAAGGCT	AlaLysAspPhel 	LysAlaLeuSerH ::: CAGGCCTTGCAGC	SerValSerLeuG	AlaAlaAlaValV.
Alignment Pred. No.: Score: Percent Si Best Local Query Matc	-096-60-sn	Oy 12	ж ж	Db 202	Oy 52	32 7		Db 382	Qy 111 Db 442	Qy 131 Db 502	Qy 151	17	Qy 190 Db 682	Qy 210 Db 742	Qy 230 Db 802	Oy 250 Db 862	Oy 270 Db 922	Qy 290 Db 982	Qy 310

	Search completed: March 15, 2003, 07:50:33 Job time : 4293 secs	rch cc time	Sea
	5 AGAACTGGGGAG 1316	1305	qq
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1304	5 ATCAAGGAGTCAGGGTTTCGTCCGTGAGGGGTTGGAGGCAGCCTGCTTCCTCCTCACCC	1245	qu
465	449 PheLysSerGluValMetValProyalLysAlaSerGlySerSerHisCys 465	449	Qy
1244	4 CICAGAACIGCCCCCIGCACCACCCCCAAGCICIAGGGCCAIGGACIGAAC	1194	Ω
448	429 GlyLysSerSerTyrCysSerGluProThrLeuLeuLysLysAlaAsnLysLysGlnAsn 448	429	ΟŸ
1193	5 CCCACAGCTGGGGGGCCAGCAGCTGGTGCTG-TCGAGACTGCTGTGTGGAGCCAGG	1135	qq
428	410 SerLeuAlaAlaGlyProCysGlyCysCysSerSerCysLeuAsnIleGlySerLys	410	Qγ
1134	1132 ACA	1132	QQ
409	390 AsnCysLeuValAsnGlySerLeuHisIleSerSerSerLeuValProMetHisGlnGly 409	390	Qy
1131	0CAGGAGGACAGGACAGGACAGCTAGCCACGGAGAGCTGCTG	1090	QΩ
389	370 LeuThrGlnLeuProCysGlnHisGlyArgArgProThrAlaProGlyGlyArgSerLeu	376	Qy
1089	6	1089	QQ
369	0 SerProGluIleThrIleThrGluAlaProValLeuAspHisSerValAlaLeuProAla	350	Qy
1089	4ACCAGC	1084	qq
349	330 ArgProGluValGluAsnArgProProGluThrGlnAlaSerGluThrSerArgProSer	330	Qγ
1083	1042 GCTACCGCTGTGGTTCGGCACATGAGGAAGCTGCAGCTGGGGC	1042	Ор

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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March 14, 2003, 13:47:15 ; Search time 7161 Seconds
    (without alignments)
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em_htgo_hum:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		% Query					
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72 17	ഹ യ	666	2474	00	BC032787		BC032787 Homo sapi
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11	504.	20.	1671	ب م	AX167589		AX167589 Sequence
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14	22	20.	1158	o w	AX167585		AX167585 Segmence
15	4	20.	1439	10	RATCAMPKAA		L26288 Rattus norv
16	489.	20.	1480	6	HUMCKI		L41816 Homo sapien
17	48	9.0	1402	10	RATPRKI		L24907 Rattus norv
10	4 0		1448	2 5	BC014825		BC014825 Mus muscu
25	2 6	17.	1032	2 5	AB00426/		AB00426/ Kattus no
21	428.	17	1332	10	D86556		D86556 Rattus norv
22	28	17.	1554	10	AF181984		AF181984 Mus muscu
23	42	17.	1032	9	AX166520		AX166520 Sequence
24	7 5	17.	1282	9	AR139102		AR139102 Sequence
25	291.	11.	1546	mı	AB021864		AB021864 Caenorhab
27	287	i -	182054	10	AL365314		AL365314 Monse DNA
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31	245	10.	2897		AXUYYYS		AXU99935 Sequence
1 m	243.	10.	1503		AX239863		AX239863 Segmence
34	243.(10.	2297		AX239861		AX239861 Sequence
35	243.	10.	3003		BC001921		BC001921 Homo sapi
36	243.	10.	3012		BC000497		BC000497 Homo sapi
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000	243	10.	3018		BC01/303		SCUI/353 HOMO Sapi
40	243.	10.	3124		AX350342		AX350342 Sequence
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KEYWORDS SOURCE		human.					
ORGANI	SM	Homo sapiens Eukaryota; M	ens Metazoa;			Craniata; Vertebra	ata: Euteleostomi:
REFERENC	Œ	ammalia;	Eutheria;			rrhini; Hominidae	; ношо.
AUTHORS	ໜ		D. and	Yoga	.A.D. and Yoganathan, T.	and their nees	
JOURNAL	7	Patent: WC	022494	7-A	3 28-MAR-2002	, cuert	0

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TEAL ALTON - "MORKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRL
TGKLFALKCIKKSPAFRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYILVMQLVSG
GELFBALLERGKYTFERDASLVIQQULSAVKYLHENIVTLEDIYESTTHYILVMQLVSG
GELFBALLERGKYTFERDASLVIQQULSAVKYLHENIVTLEDIYESTTHYILVMCLVSG
GELFBALLERGKYTERGYTERDSTVAPEVLAQKPYSKAVDCWSIGYITYILLGYPP
FYEETESKLFEKIKEGYYFESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPW
IDGNTALHEDIYESVSLOJQKNFAKSKWRQAFNAAAVHHMKKLHMNIHSPGYRFEVE
NRPPETQASETSRPSSPFITITAFAVLDHSVALPALTQLPCQHGRRPTAPGGRSLNCI
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BC032787 2474 bp mRNA linear PRI 27-JUN-2002 Homo sapiens, calcium/calmodulin-dependent protein kinase IG, clone MGC:44894 IMAGE:5179957, mRNA, complete cds.
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Submitted (06-UN0-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                   1801 CCGTGGCTCTGTGCAGTGTACGTAGATAGCTCTCGCCTGGGTCTGTGCTGTTGTCGTGA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRMR Plate: 68 Row: k Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gl: 14196444. Location/Qualifiers
Contact: nisc_mgrant.nin.gov,
Akhter,N. Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haphighi.P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
MCDWell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="calcium/calmodulin-dependent protein kinase IG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="MGC:44894 IMAGE:5179957"
/tissue_type="Brain, Lung, Testis, adult, pooled whole"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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FYEETESKLFEKIKGGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCERALSHPW
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NRGSLHISSSLVPMHGGSLAAGPCGCCSSCLNIGNKGKSSYCSEPTLLKKANKKQNFR
                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2464)
Schutte, B.C., Blork, B.C., Coppage, K.B., Malik, M.I., Gregory, S.G., Scott., D.J., Brentzell, L.M., Watanabe, Y., Dixon, M.J. and Murray, J.C. A preliminary gene map for the Van der Woude syndrome critical region derived from 900 kb of genomic sequence at 1q32-q41
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Bjork, B.C., Watanabo, Y., Murray, J.C. and Schutte, B.C.
Characterization of the human ortholog of rat CaM Kinase I (CamKig) at 1q32-q41
Unpublished
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Bjork,B.C., Watanabe,Y., Murray,J.C. and Schutte,B.C.
Direct Submission
Submitted (05-207-2001) Genetics, University of Iowa, 140
Iowa City, IA 52242, USA
Location/Qualifiers
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Isogai, T. and Yamamoto, J.

Isogai, T. and Sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA library construction: Helix Research Institute (HI) (supported by Japan Key Technology Center etc.); S. & 3'-end one pass sequencing: RAB, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

Icocation/Qualifiers
2012 bp mRNA linear PRI 15-JUL-2002 Homo sapiens CDNA FLJ38394 fis, clone FEBRA2007534, moderately similar to CamKI-like protein kinase.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens fetal brain cDNA to mRNA, clone_lib:FEBRA2
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/clone_lib="FEBRA2"
/dev_stage="fetal"
/note="cloning vector: pk
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/db_xref="taxon:9606"
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	CACCCACTACTACCTGGTCA:	8 = 8	AGTGAAATACCTACATGAGAATG	TTACCTTACCCCTGAAGAGAACTCTAAGAT 	GGAACAGAATGGCATCATGTCCACTGCCTGTGGGACC(GCTGGCCCAGAAACCTACAGCAAGGCTGTGGATTGCTGGT/ 	CATATTGCTCTGTGGATACCCCCCGTTCTATGAAGAACGGGTGTG 	GAT GAT	CAAGGACTTTATTTGCCACTTGCTTGAGAAGGATC(GGCCTTGAGTCATCCCTG	AGTCAGCCTCCAGATCCAGAAGAACTTTGCTAAGAGCAAGTGGAGG	AGCAGCT AGCAGCT	8=8	CCCTGAGATCACCATCACCGAGGCAC 	GACCCAATTACCCTGCCAGCATGG	CTGCCTGGTCAATGGCTCCCTCCACATC	CCTGGCCGGCCCTGTGGCTGCTGCTGCTGCTGCTGCTGCT	GTCC
455	339	399	459	519 695	579 755	639	669	759 935	819 995	879 1055	939	999	1059	1119	1179	1239	1299	1359
qq	QY Db	OY Db	çy D	Oy Dp	Qy Db	Qy Db	QY Db	QY	Qy Db	QQ Dp	QY Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	QQ Db	δλ

CCTTTTCTCTCTCCTTGAAAGTCCAGCACACATTCTTGTCCTTCCCCCAGTTTCCTCGCCCT 2378 GTCCTCCTACTGCTCTGAGCCCACACTCCTCAAAAAGGCCAACAAAAAACAGAACTTCAA 1594 TGGAGTCTGTCTCATTATGTGATTCCTGGAGCCTGTGCCTATGTCACTGCAATTTTCAGG CCAGCGGGGCGCCCCTCATAGGAGGCCCCAGGAGGGAGGCCCCAAGGCGTAGAAGCCTTGT 2015 GGGTCTGTGCTGTTTGTCGTGAAAAGCTTAATGGGCTGGCCAGGCTGTGTCACCTTCTCC ATGAATGACAGGCAGCTCCCCATGGTGGTCTGCCTGTGAGCTCTTCAAGTTCTAATCCTT GTTAACCTTGGAAGTTGACTATTTTAATGTCTGCCAGGAGTTCTAATCCTGCCTCTGTTC GTCGGAGGTCATGGTACCAGTTAAAGCCAGTGGCAGCTCCCACTGCCGGGCAGGCCAGAC CAGAGCAAGTGGAGCAGGGCTTAGCAGGAGCAGTTTCTGGCCAGAAGCACCAGCCTGCTG GGGTCTGTGCTGTTTGTCGTGAAAAGCTTAATGGGCTGGGCCAGGCTGTCACCTTCTCC CCACCCCTCCAGCTTCATGCTCAGTGTTGTGCTTAATAAAATGGACATATTTTTCTCT S P S Oy Ob g g g a a b b g QQ QY Db 0y 0b 0y 0y ŏ g οy Ω δy οy δy δ 70 90 QΛ

RESULT 5 HS272L161

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Gaps

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172 9

240 352 300 412 360 472 420 532 480 592 540 652 900

ORIGIN

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ACCACATGAGGAAGCTACACATGAACCTGCACAGCCCGGGCGTCCGCCCAGAGGTGGAGA 1072
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                        Length 1738
                        6
                                               5
                         ВВ
                     Score 1734.8;
Pred. No. 0;
                                               0; Mismatches
                       70.98;
99.98;
                                   Best Local Similarity 99.9
Matches 1736; Conservative
                         Query Match
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Direct Submission

Direct Submission

Submitted (21-APR-1999) E-mail contact: humquery@sanger.ac.uk

This sequence was generated from cDNA clones isolated using

sequence from the bacterial clone 272L16 (AL023754) and EST data.

The EST sequences listed match this sequence with an identity of at

least 95% between the coordinates shown.

Further information can be found at

http://www.sanger.ac.uk/HGP/Chrl/ Partial, experimentally

determined gene.

Sanger Centre name dJ272L16.C1.1.
PRI 21-APR-1999
similar to
                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST AI215131 from clone IMAGE:1925595"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(1469, .1550,1553, .1723,1721, .1738)
/note="matches EST R05661 from clone 29500"
1484. .1736
 HS272L161 1738 bp mRNA linear Human gene isolated from PAC 272L16, chromosome 1, calcium/calmodulin dependent protein kinases.
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//crganism.*Homo sapiens"

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<1. 1448

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                                                                                              Eukaryota; Metazoa; (
Mammalia; Eutheria; 1
1 (bases 1 to 1738)
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575. .650
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237. .311
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653. .777
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                                                                                     ORGANISM
           DEFINITION
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                                   ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
COMMENT
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712 99 772 780 892 840 952

us-09-960-643-1.rge

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Mus musculus, clone MGC:30513 IMAGE:4502479, mRNA, complete cds. BC021840
BC021840
MGC.
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (18-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 2416)
Strausberg, R.
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BC021840
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
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JOURNAL
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LVNGSLRISSSLVPMQQGPLATGFCCCSSCLNIGNKGKSSYCSEPTLFRKANKRQNF
KSEPWAPVRAGGSTTCRGGGTGVCLVW"
                                                                                                                                                                                               found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                    Center code: BCM HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/Link at: http://image.llnl.gov Series: IRAK Plate: 41 Row: 1 Column: 117 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210
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A Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="MGC:30513 IMAGE:4502479"
/tissue_type="Eye, retina, mouse strain C57Bl\6"
/clone_lib="NIH_MGC_94"
/lab_host="nH108"
/note="Vector: pCMV-SPORT6"
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9y Bb	871 TGTGAGAAGGCCT 888 TGCGAGAAAGCCC	TGTGAGAAGCCCTTGAGTCATCCCTGGATTGACGGAAACACGGCCTCCACCGGGACATC 930 	QY Db	35	
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Qy Db	1171 CCTGCCCTGACCC 	CCTGCCCTGACCCAATTACCCTGCCAGCGCCGCCGCCACTGCCCCTGGTGGC 1227	Qy Dp		GTCCT - ACCTC
oy Dp	1228 AGGTCCCTCAACT 	AGGTCCCTCAACTGCCTGGTCAATGGCTCCCTCCACATCAGCAGCAGCCTGGTGCCCATG 1287	oy Op		AGGAC AGG-:
Oy Db	1288 CATCAGGGTCCC 1 308 CAACAGGGCCCCC	CATCAGGGTCCCTGGCCGGCCCTGTGCTGCTCCAGCTGCTGAACATTGGG 1347	Oy B		TGTC
oy Pb	1348 AGCAAAGGAAAGT 	AGCARAGGARAGTCCTCCTACTGCTCTGAGCCCACCACAAAAAAA 1407 	Oy Db	2413	AATAJ AATAJ
Qy Db	1408 CAGAACTICAAGI 	CAGAACTICAAGTCGGAGGTCATGGTACCAGTTAAAGCCAGTGGCAGCTCCCACTGCCGG 1467 	REST AF43 LOCC	RESULT 7 AF428262 LOCUS	
Qy Db	1468 GCAGGCAGACTG 	GCAGGGCAGACTGGACTCTCATTATGTGATTCCTGGAGCCTGTGCCTATGTCACTG 1527 	ACCI VERS	ACCESSION VERSION KEYWORDS	AF.

2427 bp mRNA linear ROD 07-NOV-2001 Mus musculus calcium/calmodulin-dependent protein kinase I gamma (Camklg) mRNA, complete cds. P428262. GI:16755702 2045 GOTCTTCAAGTTCTAATCCTTAACTCCAGGATTAGCTCCCAAGTGCGCTGAGACCCA 2114 2268 AGTICTAATCCTGCCTCTGTTCCCTTTTCTCTCCTTGAAAGTCCAGCACATTCT 2353 CCAGGCTGTGTCACCTTCTCCAAGCCATATGGAGCATCTACCCAGACTCCCA 1934 TCCGTGCACACACCCAATGGAGTTAACCTTGGAAGTTGACTATTTTAATGTCTGCC 2293 CTTCCCCAGTTTCCTCGCCCTCCACCTTCAGCTTCATGCTCAGTGTTGTGCT-T 2412 IGGAATAGAAAGAAGTTCATGAGTAAGGGCTGCAAGGAATTCTTATCCTGGCCACAT 2233 regactagagaaagctgrgacrarggacrgrgagccrrcrcrcrcrgcrggcgcacac 2219 --GICICICIGIGITCIIGCCICATACCCICAGCIICGIGCICIGIGIII AGGAAGGCAGAGCAAGTGGAGCAGGGCTTAGCAGGAGCAGTTTCTGGCCAGAAGCA 1647 AGGICTCCCTGACCTGCCTGTCTATGCCCCACACCCTACGTGCCGTGGCTCTGTGC 1814 rGCACACACTCACTCCCACCTCTCAAGCCTCCAACCTCTTGGCCAGATTGGGCTCAT 1994 GTCGTTGCCTGCCCATCTGCATGAATGACAGGCAGCTCCCCATGGTGGTCTGCCTG 2054 TITCAGGAGACATATTCAACTCCTCTGCTCTTCCAAACCTGGTGTCTATCCGGCAG 1587 AGCCTTGTTGAAGCTGTGAGCAGAGAAGCGGT--------GCCCACCAGCT

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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2427)
Bjork, B.C., Watanabe, Y., Murray, J.C. and Schutte, B.C.
Characterization of the human ortholog of rat CaM Kinase I gamma
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                                                                                                                                                                                                                               University of Iowa, 140
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                                                                                                                                                                                      Schutte, B.C
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2 (bases 1 to 2427)
Bjork, B.C., Watanabe, Y., Murray, J.C. an Direct Submission
Submitted (05-0CT-2001) Genetics, Unive Iowa City, IA 52242, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                               /map="1H, 104.00 cM"
/clone="IMAGE:4502479"
/tissue_type="retina"
/note="corresponds to ES
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/gene="Camk1g"
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86. .1519
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76.1%;
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                         CAATTTTCAGGAGACATATTCAACTCCTCTGCTCTTCCAAACCTGGTGTCTATCCGGCAG 1587
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                                               1547 GACATTCCTG--GCTCTTCTCTCTCTCTGAGCTGGCATCTGCCCTGAGGGGGGGC
                                                                                                                          AGAAGCCTTGTTGAAGCTGTGAGCAGGAGAAGCGGT--------GCCCACCAGCT
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HS272L16 bn linear PRI 23-NOV-1999 Human DNA sequence from clone 272L16 on chromosome 1432.1-32.3. Contains the 3' end of the LAMB3 gene for Laminin, Beta 3 (Nicein, Ralinin, BM600) and a novel Rat ca2+/Calmodulin dependent Protein

RESULT 8 HS272L16 LOCUS DEFINITION

```
Direct Submission

Louding (27-NOV-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. Email enquiries: humquery@sanger.ac.uk CB10 15A, UK. Email enquiries: humquery@sanger.ac.uk CD10e-12, 1998 this sequence version replaced gi:3873472.

On Dec 12, 1998 this sequence version replaced gi:3873472.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence is the entire insert of clone 272L16. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272L16 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: PCTPAC2 This sequence was generated from a human chromosome 1 bacterial clone contig constructed in collaboration by the Sanger Centre chromosome 1 mapping group and Brian Schutte, Bryan Bjork, Kevin Coppage and Jeffrey Murray. Department of Pediatrics, University of Iowa, USA. Further information can be found at http://www.sanger.ac.uk/HGP/Chri.
                 genomic marker D1S491
                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                     AL033754.1 GI:4007152
HTG; BM600; ca repeat polymorphism; Ca2+/Calmodulin dependent
Protein Kinase; D1S491; Kalinin; LAMB3; Laminin Beta 3; Nicein.
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/note="MLT1A2-internal repeat: matches 358. .1643 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note='AluJo repeat: matches 101, .302 of consensus" 5536, .5966
/note="MITIAl-internal repeat: matches 5, .450 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MLT1A2 repeat: matches 23. .374 of consensus" 3677. .4074
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2347. .2925
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/note="MSTD repeat: matches 1. .426 of consensus"
1585. .1875
/note="matches 1. .319 of consensus"
1898. .2024
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/note="LTR7 repeat: matches 1. 450 of consensus"
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Catarrhini; Hominidae; Homo.
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/note="MER54B repeat: matches 486. .902 of
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rinase LIKE gene. Contains ESTs, STSs, GSSs, ger
and a ca repeat polymorphism, complete sequence.
AL023754
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6020. .6459
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/clone="RR1-27216"
/clone_lib="RPCI-1"
966. .1078
/note="MLTII repeat: matches 281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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/db_xref="taxon:9606"
/chromosome="1"
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Mammalia; Eutheria; Primates;
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. 6781	/note="MLT1A1 repeat: matches 1318 of consensus" 67866870	"MIR.	10	/note="WIR repeat: matches 68212 of consensus" 83809083	note= 084.	=="MIR	=="Alu	L2 re	"L2 re	1.19 1.1	"9 copies 4 mer acac 86% conserved" .12855	"MER91A repeat: matches 20186 of consen: .13221	peat: matches 80191 56313979)	"match: GSSs AQU/545/ AQU/6848" .14279	<pre>/note="MIR repeat: matches 60105 of consensus" 1432714442</pre>	"MIR"	"L2	-"MER5A	1.2	e="MIR	1.27	"IL2	ΞΞ"	12 re	£.	· Σ	. Σ	/note="LTR20" repeat: matches 454, .503 of consensus" 20459 20899	. <u>.</u>	"MER34	Σ.	. 7	. Σ	٠,Σ	508425193 note="MIR re	520725435 note="MIR reneat: matches 13 259 of consens	repear: marches 13239 Of Consensus 363
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Anote="Maria repeat: matches 1. 503 of consensus"

Anote="MERAAZ repeat: matches 1. 503 of consensus"

Anote="Milit repeat: matches 1. 503 of consensus"

2634. 26813

Anote="Milit repeat: matches 1. 503 of consensus"

2631. 27357

Anote="12 copies 2 mer ca 100% conserved"

27779. 27820

Anote="12 copies 4 mer caca 100% conserved"

27779. 27796. 29195

Anote="Milit repeat: matches 4. 163 of consensus"

29263. 29506. 29195

Anote="Milit repeat: matches 14. 355 of consensus"

29263. 29507

Anote="Milit repeat: matches 14. 355 of consensus"

Anote="Milit repeat: matches 14. 355 of consensus"

Anote="Milit repeat: matches 355. 618 of consensus"

Anote="Milit repeat: matches 355. 618 of consensus"

Anote="Milit repeat: matches 355. 618 of consensus"

Anote="Milit repeat: matches 1189. 1455 of consensus"

Anote="Milit repeat: matches 1189. 1455 of consensus"

Anote="Charilela repeat: matches 1125. 1189 of consensus"

Anote="Charilela repeat: matches 3488. 6190 of consensus"

Anote="Charilela repeat: matches 3451. 4317 of consensus"

Anote="Milit repeat: matches 1. 300 of consensus"

Anote="Milit repeat: ma ö
 QY
 1690
 GAGGGAGCCCCAAGGCGTAGAAGCCTTGTTGAAGCTGTGAGCAGGAGAAGCGGTGCCCCAC
 1749

 DA
 147651
 GAGGGAGCCCCAAGGCGTAGAAGCCTTGTTGTAGAGCTGTGAGCAGGAGAAGCGGTGCCCAC
 147710
 DD 147471 CCTCACTCTGAGCCCCTTTCTTGCAGGAGACATATTCAACTCCTGGTCTTCCTAGAAC 147530 7817. .38850
700c="Charliela repeat: matches 1. .1142 of consensus" 39293. .39437
700ce="MIX repeat: matches 1. .140 of consensus" complement(39554. .39839)
700ce="Match: GSS AQ070531"
71165. .41445
700ce="L2 repeat: matches 2180. .2489 of consensus" 41615. .41810 QY 1510 CCTGTGCCTATGTCACTGCAATTTTCAGGAGACATATTCAACTCCTCTGCTCTTCCAAAC 1569 QY 1570 CTGGTGTCTATCCGGCAGAGGAGGAGGAGGCAGAGCAAGTGGAGCAGGGCTTAGCAGGAGC 1629 Gaps consensus Length 157875; ó Indels .541 of 37.0%; Score 905.6; DB 9; ilarity 98.5%; Pred. No. 4.4e-239; Conservative 0; Mismatches 14; repeat: matches 68. Best Local Similarity Matches 914; Conserva repeat_region misc_feature Query Match Best Local S 1750 ōλ

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Matches 870;
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Murinae;
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                                TTCTTGTCCTTCCCCAGTTTCCTCGCCCTCCACCCTCCAGCTTCATGCTCAGTGTTGTG
                                                                                                                                      147891 TCCCACTCTGCACACACACTCCCCACCTCTCAAGCCTCCAACCTCTTGGCCAGATTGGG
                                                                                                                                                             CTCATTAATGTCGTTGCCTGCCCATCTGCATGAATGACAGGCAGCTCCCCATGGTGTCT
                                                                                                                                                                                                        GCCTGTGAGCTCTTCAAGTTCTAATCCTTAACTCCAGGATTAGCTCCCAAGTGCGCTGAG
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                      TGTGCAGTGTACGTAGATAGCTCTCGCCTGGGTCTGTGCTGTTTGTCGTGAAAAGCTTAA
                                                                   TGGGCTGGCCAGGCTGTCTCCTTCTCCAAGCAAAGCCATATGGAGCATCTACCCAGAC
                                                                                                                TCCCACTCTGCACACACTCACTCCCACCTCTCAAGCCTCCAAACCTCTTGGCCAGATTGGG
                                                                                                                                                                                                                                                      ACCCAGCCAGCACACTTCTGGCCCTTCTCCCTGCCTCAATCTAAAAGCAGTGCCACACCC
                                                                                                                            Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yokokura, H., Terada, O., Naito, Y. and Hidaka, H. Sollation and comparison of rat cDNAs encoding Ca2+/calmodulin-dependent protein kinase I isoforms Biochim. Biophys. Acta 1338 (1), 8-12 (1997)
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partial
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Eukaryota; Metazoa; Chordata;
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/note="similar to calcium/calmodulin-dependent protein
kinase I mRNA (L24907, L26288)"
/codon_start=1
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FYDEPTSEKLFERIXEGYYEERDSPFWDDISESANDFICHLLEKDPNERYTCEKALRHPW
IDGNTALHRDIYPSYSLOIGKNFAKSKWRQAFN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 813; DB 10;
Pred. No. 1.1e-213;
                  /organism="Rattus norvegicus"
/db_xref="taxon:10116"
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                                                    /clone="N5"
/tissue_type="brain"
/clone_lib="S. Nakanishi"
/dev_stage="embryo (E18)"
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90.2%;
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TGKLFAVKCIPKRALKGRESSIENETAVLRKIKHBNIVALEDIYESPNHLKIVWQLVS
GGELFDRIVERGFYTEKBASTLRQVLDAVYLHRMGIVHRDLRPBILLIYSQDEEK
IMISDFGLSKMBGKGTOWRSTACGTPGYVAPEVLAQRPYSRAVDCWSIGVIAYILLCGY
PPFYDENDSKLFEQILKAEYEFDSPYWDDISDSAKDFIRNLMEKDPNKRYTCEQAARH
PWAGDTALNKNIHESVSAQTRKNFAKSKWRQAFNATAVVRHMRKLHLGSSLDSSNAS
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4 44 C 415 g 328 t
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Homo saplens CamKI-like protein kinase mRNA, complete cds.
AF286366
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Identification and characterization of CKLiK: a novel granulocyte cast/calmodulin-dependent kinase
Blood (2000) In press
2 (bases 1 to 1579)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1579)
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/db_xref="G1:9837341"
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Pred. No. 3.2e-128;
0; Mismatches 274;
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/db_xref="taxon:9606"
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Direct Submission
Submitted (11-JUL-2000) Dept.
Medical Center Utrecht, Heidel
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                                                           Donoho,G., Scoville,J., Turner,C.A., Friedrich,G., Zambrowicz,B., Abuin,A. and Sands,A.T.
Novel human kinase proteins and polynucleotides encoding the same Patent: Wo 0142435-A 5 14-JUN-2001;
Lexicon Genetics Incorporated (US)
Location/Qualifiers
                            Eukaryoia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1671)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1074)
Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Marti
Flanagan,P. and Clary,D.S.
Novel human protein kinases and protein kinase-like enzymes
Patent: WO 0189503-A 8 31-MAY-2001;
Sugen, Inc. (US)
                 AAAACCITCATTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTTTTCCTGGTG
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AX166517
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I (bases 1 to 1074)

Donoho,G., Scoville,J., Turner,C.A., Friedrich,G., Zambrowicz,B., Abuin,A. and Sands,A.T.

Novel human kinase proteins and polynucleotides encoding the same Patent: Wo 0142435-A 3 14-JuN-2001;
Lexicon Genetics Incorporated (US)
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AAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTTTTCCTGGTG 189
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                                              GAGTCTCCATTCTGGGATGACATTTCTGAGTCAGCCAAGGACTTTATTTGCCACTTGCTT
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PAT 03-JUL-2001

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1158 bp Sequence 1 from Patent W00142435. AX167585 AX167585.1 GI:14596986

DEFINITION ACCESSION VERSION KEYWORDS

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Donboo, G., Scoville, J., Turner, C.A., Friedrich, G., Zambrowicz, B., Abuin, A. and Sands, A. I.
Novel human kinase proteins and polynucleotides encoding the same Patent: Wo 0142435-A 1 14-JUN-2001,
Lexicon Genetics Incorporated (US)
Location/Qualifiers
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                                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Catarrhin; Hominidae;
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Pred. No. 1.4e-127;
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    nucleic search, using frame_plus_p2n model

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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ALIGNMENTS

Human polynucleotide SEQ ID NO 4692. BP AA160703 standard; cDNA; 1956 (first entry) 22-OCT-2001 AA160703; RESULT 1

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia; ss

Homo sapiens

245 CGGGACAGCAGCCTGGAGAATGAGATTGCTGTTGAAAAAGATCAAGCATGAAAACATT

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, Immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as latheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and c.N.S disorders.
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Zhang J;
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Xue AJ,
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Goodrich R, Drmanac RT;
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SerbeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIleVal
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The invention relates to a method for screening biologically active agent that modulates cancer associated protein kinase function. The invention also relates to a method for diagnosing cancer comprising determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase. The method is useful for diagnosing cancer. A protein kinase is useful for screening biological agents that modulate cancer associated protein kinase function. Downregulating the activity of protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon cancer. A nucleic acid encoding protein kinase is useful to screen biopsy cancer. A nucleic acid encoding protein kinase is useful to screen biopsy cancer. A nucleic acid encoding protein kinase is useful to screen biopsy amplified DNA in the cell or increased expression of corresponding mRNA amplified DNA in the cell or increased expression of corresponding mRNA corp is a molecular weight, amino acid and nucleotide sequences between the two cells. The present sequence is human calmodulin kinase CAMK-XI gene corp.
                                                                                                                                                                                                                                                                                                           Human; cytostatic; antisense gene therapy; screening; protein kinase;
cancer; liver; colon; tumour; inflammation; arthritic synovium; CAMK-X1;
calmodulin kinase; enzyme; gene; chromosome 1q32.1-32.3; ds.
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LysLysAlaAsnLysLysGlnAsnPheLysSerGluValMetValProValLysAlaSer
                1385 AAAAAGGCCAACAAAAAACAGAACTTCAAGTCGGAGGTCATGGTACCAGTTAAAGCCAGT
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, Xu C, Xue AJ,
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Wehrman T, Xu
Goodrich R,
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2000US-0552317.
2000US-0598042.
2000US-062312.
2000US-0653450.
2000US-0662191.
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2000US-0727344
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03-AUG-2000; 2
14-SEP-2000; 2
19-OCT-2000; 2
29-NOV-2000; 2
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25-APR-2000;
09-JUL-2000;
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immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic atteral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
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                                                                                                                                The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic.
                                      disorders
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Conservative:
Mismatches:
                                    Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                            NO 1120; 10078pp; English.
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Best Local Similarity:
Query Match:
DB:
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P-PSDB; AAM39761
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                                                                      GlyTyrTyrGluPheGluSerProPheTrpAspAspIleSerGluSerAlaLysAspPhe
                                                                                            IleCysHisLeuLeuGluLysAspProAsnGluArgTyrThrCysGluLysAlaLeuSer
                                                                                                                   HisProTrplleAspGlyAsnThrAlaLeuHisArgAspIleTyrProSerValSerLeu
                                                                                                                                         GlnIleGlnLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsnAlaAlaAlaVal
                                                                                                                                                               ValHisHisMetArgLysLeuHisMetAsnLeuHisSerProGlyValArgProGluVal
                                                                                                                                                                                     GluAsnArgProProGluThrGlnAlaSerGluThrSerArgProSerSerProGluIle
                                                                                                                                                                                                           354 ThrileThrGluAlaProValLeuAspHisSerValAlaLeuProAlaLeuThrGlnLeu
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leukaemia;
                                 Human; receptor; diagnostic; therapeutic; gene therapy; vaccine cell proliferative disorder; Crohn's disease; lymphoma; leukaem acquired immune deficiency syndrome; AIDS; autoimmune disorder;
Human diagnostic and therapeutic polynucleotide (DITHP) #29.
                                                                                                                                                                                                                                                                          20000S-0184697.
20000S-0184698.
20000S-0184769.
20000S-0184770.
20000S-0184771.
20000S-0184771.
20000S-0184773.
20000S-0184773.
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2000US-0184797
                                                                                      respiratory disorder; ss
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15-MAY-2000;
16-MAY-2000;
16-MAY-2000;
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(INCY-) INCYTE GENOMICS INC

Jones AL; , Daffo A; Chang SC; Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang Chen A, D'Sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE; Dufour GE, Flores V, Fong WT, Greenawalt LB, Hillman JL, Jiu TF, Rosberry AM, Rouse BH, Russo FD, Stockdreher TK, Waright RJ, Yap PE, Yu JY, Braddey DL, Bratcher SR, Chen W; Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;

2001-502867/55. P-PSDB; AAU19443

Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics

Claim 1; Page 310-311; 522pp; English.

The invention relates to polynucleotides (I) encoding diagnostic and therapeutic (DTHP) polypeptides (II), which include e.g. enzymes, and proteins involved in growth and development and receptors. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate DTHP expression. For example, (I) and (II) may be used to treat disorders associated with decreased polypeptide expression by rectifying mutations or deletions in a patient's genome,

that affect the activity of the DITHPS, by expressing inactive proteins or supplementing the patient's own production of them. (1) and (11) may be used to treat diseases, for example, cell proliferative disorder, crohn's disease, acquired immune deficiency syndrome (AIDS). Jumphoma, leuwaemia, autoimmune disorders, and respiratory disorders. Additionally, (1) may be used to produce the DITHPS, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therefore which patients may be in need of restorative careapy. (11) may also be used as antipodies and antagonists may also be used as diagnostic agentify modulators of DITHP expression and activity. The anti-DITHP antibodies and antagonists may also be used as diagnostic agents for detecting the presence of DITHPP is samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAS30986-AAS31196 represent human diagnostic and therapeutic (DITHP) polynucleotides of the invention. 828888888888888888888888

Sequence 2689 BP; 642 A; 748 C; 678 G; 621 T; 0 other;

Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 7.06e-190 2327.50 95.86% 95.24% Percent Similarity: Best Local Similarity: gnment Scores: Query Match: DB: .. Q

US-09-960-643-2 (1-476) x AAS31014 (1-2689)

356 476 ValThrLeuGluAspIleTyrGluSerThrThrHisTyrTyrLeuValMetGlnLeuVal 100 536 596 160 716 180 176 200 836 SerGlyGlyGluLeuPheAspArgIleLeuGluArgGlyValTyrThrGluLysAspAla 120 40 80 ArgAspSerSerLeuGluAsnGluIleAlaValLeuLysLysIleLysHisGluAsnIle MetlleThrAspPheGlyLeuSerLySMetGluGlnAsnGlyIleMetSerThrAlaCys GlyThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLysAlaVal LysThrPheIlePheMetGluValLeuGlySerGlyAlaPheSerGluValPheLeuVal ATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGGCATCATGTCCACTGCCTGT Н 237 297 41 357 117 101 597 717 181 21 61 81 477 537 121 141 657 161 777 g 셤 a g 셤 g a qq ò ò οy 8 ŏ δ à 8 ò à ò ò

AspCysTrpSerIleGlyValIleThrTyrIleLeuLeuCysGlyTyrProProPheTyr 220

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cancer; allergy; sarcoma, leured; acquired immune deficiency syndrome, AIDS; Addison's disease; microbial infection; inflammation; osteoporosis; atherosclerosis; cardiovascular disease; myocardial infarction; anaemia; myasthenia gravis; cartrhosis; cataract; growth and development disorder; seizure disorder; pulmonary embolism; Gaucher's disease; lipid disorder; lipid storage disease; Pick's disease; Tay-Sachs disease; lipid disorder; asthma; obesity; restorative therapy; cytostatic immunomodulatory; antimicrobial; cardiovascular; antimiflammatory; vaccine; ss. Human kinase; PKIN; gene therapy; adenocarcinoma; immune disorder; gout; 1436 1136 1196 1316 OVALLEUASPHISSERVALALALEUPROALALEUThrGlnLeu---ProCysGlnHisGl 378 418 GATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCCCCCATTCTAT AspProAsnGluArgTyrThr-CysGluLysAlaLeuSerHisProTrpIleAspGlyAs LeuHisMetAsnLeuHisSer-ProGlyValArgProGluValGluAsnArgProProGl uThrGlnAlaSerGluThrSerArgProSerSerProGluIleThrIleThrGluAlaPr slleSerSerSerLeuValProMetHisGlnGlySerLeuAlaAlaGlyProCysGlyCy GluGluThrGluSerLysLeuPheGluLysIleLysGluGlyTyrTyrGluPheGluSer ВЪ standard; cDNA; 1736 Human kinase (PKIN)-2 cDNA 18-DEC-2001 (first entry) AAD18817; AAD18817 1077 1377 1557 1017 1137 1197 1257 1317 378 1437 1497 438 221 897 261 280 320 339 359 398 418 RESULT 5 AAD18817 g ΩD Q ΩD ŏ g δy Q δy qq ŏ g δ QQ ŏ g ò Dp δ ρp δ ò δy οy Ω g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human kinases (PKIN) and the nucleic acids encoding them. PKIN is used as vaccine and in gene therapy. PKIN is used in the prevention, diagnosis and treatment of diseases cancers, adenocarcinoma, leukaemia, sarcoma, immune disorder, Addison's disease, adenocarcinoma, leukaemia, sarcoma, immune disorder, Addison's disease, adenocarcinoma, leukaemia, sarcoma, immune disorder, Addison's disease, advorable inflammation, myasthenia gravis, cardiovascular disease and/or inflammation, myasthenia gravis, atherosclerosis, cirrhosis, osteoporosis, myocardial infarction, cataract, growth and development disorder, seizure disorder, pulmonary embolism, Gaucher's disease, lipid disorder, ilpid storage disease, plick's disease, Tay-Sachs disease, renal disease and obesity. PKIN may be used to treat disorders associated with decreased PKIN capterssion by rectifying mutations or deletions in a patient's genome that affect the activity of PKIN by expressing inactive proteins or to supplement the patients own production of PKIN PKIN nucleic acids may be used to produce the PKIN POlypeptide, by inserting the nucleic acids may be used and its complementary sequences may also be used as DNA probes in considering and consider and quantitate the presence of similar and considering the cell and quantitate the presence of similar and considering the cell and quantitate the presence of similar and considering the cell and quantitate the presence of similar and considering the cell and quantitate the presence of similar and considering the cell and quantitate the presence of similar and considering the cell and quantitate the presence of similar and considering the cell and quantitate the presence of similar and considering the cell and quantitate the presence of similar and considering the cell and quantitate the presence of similar and considering the cell and quantitate the presence of similar and considering the cell and quantitate the presence of similar and considering the cell and considering the ce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yue H, Gandhi AR, Tribouley CM, Kearney L, Griffin JA, Nguyen DB;
Bandman O, Lu DAM, Lal P, Burford N, Khan FA, Walia NK, Yao MG;
Patterson C, Burrill JD, Marcus GA, Zingler KA, Recipon SA, Lu Y;
Policky JL, Thornton M, Tang YT, Hafalia A, Elliott VS, Baughn MR;
Walsh RT, Ramkumar J, Borowsky ML, Au-young J, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= c
/product= "Mature human PKIN-2 protein"
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                                                                                                                                     "Human PKIN-2 protein"
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                                                 Location/Qualifiers
159..1232
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28-APR-2000; 2000US-200226P.
05-MAY-2000; 2000US-20339P.
11-MAY-2000; 2000US-203564P.
26-MAY-2000; 2000US-205564P.
26-MAY-2000; 2000US-2075739P.
01-JUN-2000; 2000US-208795P.
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279..1229
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P-PSDB; AAE11768.
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Walsh RT, Ran
Gururajan R;
Homo sapiens
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1736 272 63 110 90

Matches: Conservative: Mismatches: Indels:

1.22e-97 1250.50 62.85% 51.03%

Percent Similarity: Best Local Similarity:

Score: Pred.

Query Match:

Length:

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|GGTGACACACCCCTCAACAAAAACATCCACGAGTCCGTCAGCGCCCAGATCCGGAAAAAC 1058
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                                                         AlaValAspCysTrpSerIleGlyValIleThrTyrIleLeuLeuCysGlyTyrProPro
                                     MetGlyArgLysGluGluAspAspCysSerSerTrpLysLysGlnThrThrAsnIleArg
                                                                                                               LysThrPheIlePheMetGluValLeuGlySerGlyAlaPheSerGluValPheLeuVal
                                                                                                                                                                                             LysGlnArgLeuThrGlyLysLeuPheAlaLeuLysCysIle---LysLysSerProAla
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US-09-960-643-2 (1-476) x AAD18817 (1-1736)
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Nucleic acids encoding human kinase polypeptides, useful for preventing
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                                                                                                 Human; protein kinase; PTK; STK; cancer; cardiovascular disease; metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease; reproductive disorder; gene therapy; ss.
1417 GAGGACTGTTTGAGTTCAGGAGTTTTAAGACCAGCCTGACCAACATGGTGAAACCCCATC 1476
                                                                                                                                                                                                                                                                                                                                                -----AATGAGCTGAGATCACACCACTGC 1608
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                                                          1238 AA-GACGAGCCTGGGGTGGAGAGGAGCCGGCATCTGCCGAGCACCTCCTGTTTGCC
                                                                                                                                                      1357 CACTGGGCCGGGTGCAGTGGCTCACGCCTGTAATCCCAACACTTTGGGAGGCTGAGGCAG
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                                                                                 ------teuThrGlnLeuProCys-----
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                                                                                                                                 -----GluHis---GlyArg
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                                   356 ThrGluAlaProValLeuAspHisSerValAlaLeuProAla
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Clary D;
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Flanagan P,
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Inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoietic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. dathana), inflammatory disorders (e.g. asthana), infectious disease (e.g. HIV) and reproductive disorders (e.g. infectious Additionally, polynucleotides encoding protein kinases may be abed for gene therapy and as DNA probes in diagnostic assays.

The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify
                                                                        AASO6701-AASO6757 encode for novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polynucleotides encoding protein kinases and the polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178
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diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections -
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                                                                                                                                                                                                                                                                                                                                                           Sequence 1074 BP; 313 A; 258 C; 276 G; 227 T; 0 other;
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233
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45
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Matches:
Conservative:
Mismatches:
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                                             Example 1; Figure 1; 433pp; English.
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1246.00
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The present sequence encodes a kinase polypeptide. The kinase polynucleotides and polypeptides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for the detection of mutant kinases, or inappropriately expressed kinases for the diagnosis of a disease or disorder. They are useful for screening for drugs (or high throughput screening of combinatorial libraries) effective in the treatment of symptomatic or phenotypic manifestations of that disease or disorder. The polynucleotide sequence is useful as a source of probes and primers, which can be used to screen libraries, isolate
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The present sequence encodes a kinase polypeptide. The kinase polynucleotides and polypeptides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for the detection of mutant kinases, or inappropriately expressed kinases for the diagnosis of a disease or disorder. They are useful for screening for drugs (or high throughput screening of combinatorial libraries) effective in the treatment of symptomatic or phenotypic manifestations of that disease or disorder. The polynucleotide sequence is useful as a source of probes and primers, which can be used to screen libraries, isolate clones, and prepare cloning and sequencing templates.
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Human kinase; PKIN; gene therapy; adenocarcinoma; immune disorder; gout; cancer; allergy; sarcoma; leukaemia; acquired immune deficiency syndrome; AIDS; Addison's disease; microbial infection; inflammation; osteoporosis; atherosclerosis; cardiovascular disease; myocardial infarction; anaemia;
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85.49%
73.15%
49.58%
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/product= '
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              LysLeuHisMet 322
                                                 961 AAACTACACCTC 972
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ABL60905

XX

AC

ABL6

XX

ABL6

ABL6

XX

ABL6

ABL6

ABL6

ABL7

AB
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us-09-960-643-2.p2n.rng

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myasthenia gravis; cirrhosis; cataract; growth and development disorder; setzure disorder: pulmonary embolism; Gaucher's disease; lipid disorder; lipid storage disease; pick's disease; ray-Sachs disease; renal disease; obesity; restorative therapy; immunomodulatory; vaccine; cardiovascular; antimicrobial; cytostatic; antiinflammatory; asthma; ss.
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Homo sapiens

Location/Qualiflers
19..126
/*tag= a
/product= "Human PKIN-11 protein" Key CDS

WO200181555-A2

01-NOV-2001

20-APR-2001; 2001WO-US12992

28-APR-2000; 05-MAY-2000; 11-MAY-2000; 20-APR-2000;

2000US-202339P. 2000US-203505P. 2000US-205564P. 2000US-207739P. 2000US-208795P. 18-MAY-2000; 26-MAY-2000;

(INCY-) INCYTE GENOMICS INC

01-JUN-2000;

Yue H, Gandhi AR, Tribouley CM, Kearney L, Griffin JA, Nguyen DB; Bandman O, Lu DAM, Lal P, Burford N, Khan FA, Walia NK, Yao MG; Patterson C, Burrill JD, Marcus GA, Zingler KA, Recipon SA, Lu Y; Policky JL, Thornton M, Tang YT, Hafalia A, Elliott VS, Baughn MR; Walsh RT, Ramkumar J, Borowsky ML, Au-young J, Hillman JL; Policky JL, Thornton M Walsh RT, Ramkumar J, Gururajan R;

WPI; 2001-611740/70. P-PSDB; AAE11777.

Human kinases and nucleic acids, useful for preventing diagnosing and treating cancers, inflammation and immune disorders –

Claim 5; Page 159; 166pp; English.

cids encoding them. PRIN is used as vaccine and in gene therapy. PRIN is used in the prevention, diagnosis and treatment of diseases cancers, adecorationan, leukaemia, sarcoma, immune disorder, Addison's disease, adecorationan, leukaemia, sarcoma, immune disorder, Addison's disease, adenoration deficiency syndrome (AIDS), anaemia, asthma, allargies, gout, microbial infections, cardiovascular disease and/or inflammation, infarction, cataract, growth and development disorder, seizure disorder, plumonary embolism, Gaucher's disease, lipid disorder, ipid storage disease, plck's disease, Tay-Sachs disease, renal disease and obesity. PRIN may be used to treat disorders associated with decreased PRIN expression by rectifying mutations or deletions in a patient's genome that affect the activity of PRIN by expressing inactive proteins or to used to produce the PRIN polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. PRIN nucleic acids and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples and therefore which patients may be nucleic acid sequences in samples and therefore which patients may be nucleic acid in need of restorative therapy. The present sequence is human PRIN-11 The present invention relates to human kinases (PKIN) and the nucleic

Sequence 1661 BP; 408 A; 452 C; 448 G; 353 T; 0 other;

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Length:
Matches:
Conservative:
Mismatches:
          2.79e-97
1246.00
85.49%
73.15%
                                 Percent Similarity:
Best Local Similarity:
Alignment Scores:
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	Query DB:	Mat	ch:	49.58% 22	Indels: Gaps:	2.2	
	60-SN	-096-6	-643-2 (1-476)	x AAD18826 (1-	1661)		
	oy da	1 150	MetGlyArgLysG ::: 	GluGluAspAspCysSolusis:::	erSerTrpLysLys 	GlnThrThrAsnIleArg	20
	3 ,	י כ			21CC19GAAAAAAA	chadel of the state of the	1
	å f	219	LysThrPhellePI AGATCTTCGAGT		1yserG1yA1aPnese ::: GAACCGGGGCCTTTT	SerGiuvaiPheLeuvai CCGAAGTGGTTTTAGCT	278
	3 6	•					
	op Op	279	Lyselinighed ::::::: GAAGAGAAGGCAA		::: STGAAGTG		n (1)
	δý	9	JASE	uGluAsn	eAlaValLeuLy	lleLysHisGluAs	7
	qq	339	::::::::::::::::::::::::::::::::::::::	:::		:	
	ΟŅ	80	levalThrL	TyrGluS	SThrThrHisTy	vrLeuValMetGlnLe	6
	QQ	399	ATTGTTGCCCTGG			PACTTGGTCATGCAGCTG	4
	δy	100	ValSerGlyGlyG	.yGluLeuPheAspArgIleLeu	leLeuGluArgGlyValTy	ValTyrThrGluLysAsp	1
	QQ	459	STCCGGTGG	H	TAGTGGAGAAGGGG	TAC	518
	ογ	7	AlaSerLeuVall	llleGlnGlnValLeuS	SerAlaValLysTyr	AS	13
	ορ	519	CCAGCACTCT	CCCCAAGTCTTG	GTGTACT	TCCACAGAATGGGCAT	578
	ΟŊ	140	ValHisArgAspLeuLys	ceuLysProGluAsnLeuLe	uTyrLeuThr		159
	QQ	579	- SS	-ပ္ပ	GTACTACAGT	AAGATGAGGAGTC	9
	δλ	160		AspPheGlyLeuSerLysMe	tG1uG]	<pre>lnAsnGlyIleMetSerThr { ::: </pre>	17
	QQ	639	ATGATCAGT	CTTTGG	GGAGG	ATGTGATGTC	869
	ΟŊ	7	AlaCysGlyThrProGl	YTYTVALALA	ProGluValLeuAlaGlnI	SlnLysProTyrSerLys	19
	qq	669	GTC	CTATGTCGC	CCIC	AACCTTAC	75
	ΟŊ	6	AlavalAspCysT	'sTrpSerIleGlyValI		euLeuCysGlyTyrProPro	21
	Ωp	759	Ħ	TCGGAGT	CATC	SCGCTACCCTCC	818
	δy	219	PheTyrGluGluThrGluS	ThrGluSerLysLeuPheG	lurysilety	sGluGlyTyrTyrGluPhe	23
	qq	819	TTTA	AATGACTCCAAGCTCT	AGCAGATCCT	SCGGAATATGAGTT	878
	ΟŊ	239	GluSerProPheT	OPheTrpAspAspIleSerG	GluSerAlaLysAspPheI	leCysHisLeuLe	~
	QQ	879	CTCC	TCTCC	ACTCTGCAAAAGAC	ттсевласства	938
	Qy	259	GluLysAspProP	roAsnGluArgTyrThrCy	SGluLys	SerHisProTrpIleAsp	278
	ΟD	939	AGAAGGACC	CACGT	110	CACCCATGGAT	866
	δy	279	lyAsnThrA	- 달	leTyrProSerValSer	erLeuGlnIleGlnLysAsn	298
_	QQ	666	TGACACAG	CCTCAACAAAACATCC	CGTCA	CAGATCCGGAA	1058
	οy	299	PheAlaLysSerI	GerLysTrpArgGlnAlaP	SinAlaPheAsnAlaAlaAla'	aValValHisHisMetArg	31
	QQ	1059	AAGA	AGAG	၁၅၅၁	CGTGAGACATATGAG	1118
	ΟŊ	319	LysLeuHisMet	322			
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                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a kinase polypeptide. The kinase polynucleotides and polypeptides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for the detection of mutant kinases, or inappropriately expressed kinases for the diagnosis of a disease or disorder. They are useful for screening for drugs (or high throughput screening of combinatorial libraries) effective in the treatment of symptomatic or phenotypic manifestations of that disease or disorder. The polynucleotide sequence is useful as a source of
                                                                                                                                                                                                                                                                                        Novel isolated human kinase polynucleotide that shares structural similarity with animal kinases including calcium/calmodulin-dependent protein kinases and serine/threonine protein kinases, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346
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                                                                                                                                                                                                                                                                                                                                                                                                                                            primers, which can be used to screen libraries, isolate d prepare cloning and sequencing templates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysThrPheIlePheMetGluValLeuGlySerGlyAlaPheSerGluValPheLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetGlyArgLysGluGluAspAspCysSerSerTrpLysLysGlnThrThrAsnIleArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1671 BP; 453 A; 437 C; 448 G; 333 T; 0 other;
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274
60
97
91
                                                                             Nucleotide sequence of a human kinase polypeptide
                                                                                                 human disease; human disorder; ss.
                                                                                                                                                                                                                                          Friedrich G,
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 32; 32pp; English.
                    ВР
                                                                                                                                                                                                                                          Turner
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                    AAH25120 standard; DNA; 1671
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1246.00
64.35%
52.79%
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                                                           (first entry)
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Sands AT;
                                                                                                                                                                                                                                                                      2001-381667/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                 Human; kinase;
                                                                                                                                       WO200142435-A2
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|1305 AGGCGCTTTCTATACTTAATCCCATGTCATGCGACCCTAGGACTTTTTTAACATGTAAT 1364
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GGCAAGGAAAGCAGCATAGAGAATGAGATAGCCGTCCTGAGAAAGATTAAGCATGAAAAT 406
                                                                                                                                                                                                                                     ValHisArgAspLeuLysProGluAsnLeuLyrLeuThrProGluGluAsnSerLys 159
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                                                                                                AlaSerLeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIle
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                              IleValThrLeuGluAspIleTyrGluSerThrThrHisTyrTyrLeuValMetGlnLeu
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous localised neuropathkes and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
                                                                                                                                         Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                          1485 TCTACTAAAATATAAAAATTAGCCGGGTGTGGTGGCGAGCACCTGTAATGTCAGCTACTT 1544
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-GlyGlyArgSerLeuAsnCysLeuValAsn
                                                                                                             ProCysGlyCysCysSerSerCysLeuAsnIleGlySerLysGlyLysSerSerTyrCys
                                                       GlySerLeuHisIleSerSerSerLeuValProMetHisGlnGlySerLeuAlaAlaGly
                                                                                                                                                                                             ----ThrLeuLeuLysLysAlaAsnLysLysGln 447
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Zhang J;
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Yang Y,
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Xu C, Xue AJ,
), Drmanac RT;
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such as central nervous system injuries
                                                                                 1545 GGGAGGCTGAGGCA-GGAGAATCGCTTGAGCCC
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Wehrman T, Xu
Goodrich R,
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2000US-0653450.
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2000US-0693036.
2000US-0727344.
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J, Wang Z, W
QA, Zhou P,
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03-AUG-2000;
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29-NOV-2000;
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lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemoteactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                      The sequence data for this patent did not form part of the printed
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                                                                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Humrington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                               GlyAsnThrAlaLeuHisArgAspIleTyrProSerValSerLeuGlnIleGlnLysAsn
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Zhang
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Yang Y,
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u C, Xue AJ,
Drmanac RT;
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25-APR-2000; 2000US-0552317.
9-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653450.
19-CT-2000; 2000US-0653450.
29-NOV-2000; 2000US-053344.
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Wang Z,
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Wang J, W
Zhao QA,
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utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                           assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                           form part of the printed
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| ATAATGATCAGTGACTTTGGATTGTCAAAAATGGAGGGCAAAGGAGATGTGATGTCCACT
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                                                                                                                        T; 0 other;
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Conservative:
Mismatches:
Indels:
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                                                                                                                        C; 462 G; 365
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                                                                           this
                                                                                                                        Sequence 1733 BP; 439 A; 467
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1243.00
85.49%
72.84%
                                                                           Note: The sequence data for
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Best Local Similarity:
                                                                                           specification
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                                                                                                                                                                                     Score:
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The present sequence is the coding sequence for Murine Dendritic Cell Kinase 3 (MDCK-3). The protein encoded by the present sequence is useful for treating a variety of disorders listed in the disclosure of the specification, including autoimmune disorders, allergic reactions, myeloid or lymphoid cell deficiencies, wound healing and tissue repair and replacement, burns, inclisions and ulcers, periodonical disease, inflammatory diseases, tumours and bacterial, viral or fungal infection. MDCK-3 is a member of the Ca2+/calmodulin-dependent kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammations, infections, tumors, allergies, autoimmune diseases, and for stimulating or suppressing immune responses
                                                                                        1055 GGTGACACACCCTCAACAAAACATCCACGAGTCCGTCAGCGCCCAGATCCGGAAAAC 1114
                                                                                                                                                                                                                                                                                                                               Murine; Dendritic Cell Kinase; MDCK-3; autoimmune disorder; allergy; wound healing; periodontal disease; inflammatory disease; tumour; infection; Ca2+/calmodulin-dependent kinase family; ss.
                                      GlyAsnThrAlaLeuHisArgAspIleTyrProSerValSerLeuGlnIleGlnLysAsn
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258
52
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Matches:
Conservative:
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Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-960-643-2 (1-476) x AAC90432
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1238.50
68.74%
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P-PSDB; AAB50055.
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           IleMetIleThrAspPheGlyLeuSerLysMetGluGlnAsnGly---IleMetSerThr
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| ATAATGATCAGTGACTTTGGCTTGTCGAAAAATGGAGGGCAAAGGAGGTGTGATGTCCACG
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                                                                                            ValHisArgAspLeuLysProGluAsnLeuLeuTyrLeuThrProGluGluAsnSerLys
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MetGlyArgLysGluGluAspAspCysSerSerTrpLysLysGlnThrThrAsnIleArg
                                                                                  LysGlnArgLeuThrGlyLysLeuPheAlaLeuLysCysIle---LysLysSerProAla
                                                                                                                         PheArgAspSerSerLeuGluAsnGluIleAlaValLeuLysLysIleLysHisGluAsn
                                                                                                                                                               IleValThrLeuGluAspIleTyrGluSerThrThrHisTyrLeuValMetGlnLeu
                                                                                                                                                                           AlaSerLeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIle
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                                         LysThrPheIlePheMetGluValLeuGlySerGlyAlaPheSerGluValPheLeuVal
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Human; death domain-containing receptor; DDCR; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; varuoide; fungicule; opthalmological; gene therapy; immunodeficiency disease; Acquired immune deficiency syndrome; ADDS; leukaemia; autoimmune disease; systemic lupus erythematosus; hyperproliferative disorder; neoplasm; cerebrovascular disorder; cerebral ischaemia; angiogenesis; cardiovascular disorder; neurodegenerative disease; Alcheimer's disease; Parkinson's disease; neurodegenerative disease; Alcheimer's disease; SMA; apoptosis; spinal muscular atrophy; epithelial cell proliferation; infection; cancer; wound healing; skin aging; chemotaxis; HDPVZ91 clone; ss.
                                                                                                                                                   1484
                                                                           1368 CACCACTGTGACAACAGGGCACACTGGAAGCAAGTGACCCGGCTCTGGAGGTGGAACCCA 1427
                                                                                                                                                                                                                   1308 TAGTITCCTITCTTCTTCGTCGGGGTCGCAGGATTCGGAGCTGAGAGGAGCCCAGGCC 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New death-domain containing receptor polynucleotides and polypeptides, useful for treating and diagnosing cancer
                                                                                                                  394
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human death domain-containing receptor (DDCR) cDNA from HDPV291 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s and their corresponding proteins. DDCR cDNA and protein are to prevent, treat or ameliorate a medical condition in mammals.
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                                              ---Pro
                                                                                                             375 CysGlnHisGlyArgArgProThrAlaProGlyGlyArgSerLeuAsnCysLeuValAsn
                                                                                                                                               1428 GGGGGCAGGGCCGGGGAAGGAGAAGCCCCT---GGCCGGAGCAGCTCCTGCATCAGAAAC
                                                                                                                                                                                 395 GlySerLeuHisIleSerSerSerLeuValProMetHisGlnGlySerLeuAlaAlaGly
                                           359 ProvalLeuAspHisServalAlaLeuProAlaLeuThrGlnLeu
                                                                                                                                                                                                                                                                         415 ProCysGlyCysCysSerSerCysLeuAsnIle 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
288..1130
                                                                                                                                                                                                                                                                                                                                                        AAD04775 standard; cDNA; 1578 BP
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They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The DDCR protein and its antibodies are used in the diagnosis and treatment of disorders such as immunodeficiency diseases (e.g. Acquired immune deficiency such as immunodeficiency diseases (e.g. Acquired immune deficiency syndrome (AIDS), leukaemia) autoimmune diseases (e.g. systemic lupus erythematosus, rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of the breast or liver), cerebrovascular disorders (e.g. cardiac arrest), neurodegenesis), cardiovascular disorders (e.g. cardiac arrest), neurodegeneative diseases (e.g. Alzheimer's disease, Parkinson's disease), ocular disorders (e.g. corneal infection), degenerative diseases (e.g. spinal muscular atrophy-SMA), cancer, aberrant apoptosis, disorders of the placenta or uterus and infections caused by bacteria, viruses and fungi. The DDCR proteins to prevent skin aging due to sunburn, to maintain organs before transplantation, to support cell culture of primary tissues, to regenerate tissues and in chemotaxis. The DDCR sequences are used in correcting aberrant cellular apoptosis by gene therapy.

The present sequence is human death domain-containing receptor (DDCR) CDCR) CDNCR (CDNCR) CDNCR) CDNCR (CDNCR) CDNCR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 GlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIleValHisArgAspLeuLys
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Matches:
Conservative:
Mismatches:
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Search completed: March 15, 2003, 05:11:17 Job time : 344 secs

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March 14, 2003, 17:30:16; Search time 182 Seconds (without alignments) 9436.615 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

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11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

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14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 4, Appli	7	1,	46,	Sequence 7, Appli	വ	Sequence 189, App	Sequence 47, Appl	Sequence 48, Appl	Sequence 49, Appl	Sequence 177, App	Sequence 6, Appli		Sequence 1, Appli	Sequence 45, Appl		9		Sequence 44, Appl
ID	US-09-935-464-4	US-09-935-464-2	US-09-935-464-1	US-09-935-464-46	US-09-935-464-7	US-09-935-464-50	US-09-764-868-189	US-09-935-464-47	US-09-935-464-48	US-09-935-464-49	0 US-09-731-872-177	US-09-935-464-6	US-09-796-692-7777	0 US-09-817-181-1	US-09-935-464-45	0 US-09-971-118-5	0 US-09-971-118-6	US-09-935-464-43	US-09-935-464-44
% Query Match Length DB	1738 9	1383 9	157875 9	480 9	501 9	319 9	476 9	467 9	470 9	356 9	1361 1(386 9	474 9	1372 10	27 9	25 1(31 1(23 9	23 9
% Query Match L	6.99	9.09		18.9	18.4	13.0	11.2	8.7	8.5	9.7	6.1	3.3	1.3	1.3	1.1	1.0	1.0	6.0	6.0
Score	1636	1239	803	462	450	319	274	212	209	185	149	80	32	32	27	25	25	23	23
Result No.	П	7	m	4	S	9	7	œ	σ	10	11	12	c 13	14	15	c 16	c 17	18	19

Sequence 103, Appl Sequence 15, Appl Sequence 56, Appl Sequence 39, Appl Sequence 54, Appl Sequence 54, Appl	18, 9 96, 9 206, 8 8, 5, A	Sequence 7, Appli Sequence 3, Appli Sequence 621, App Sequence 621, App Sequence 9, Appli Sequence 9, Appli	40248
0S-10-114-893-103 10 US-09-839-185-15 9 US-09-935-464-56 9 US-09-935-464-39 9 US-09-935-464-53 9 US-09-935-464-54 9 US-09-935-464-54	9 US-09-935-464-18 10 US-09-770-791-570 10 US-09-770-445-96 10 US-09-778-844-206 10 US-09-985-675-8 9 US-09-123-490-9	10 US-09-985-675-7 10 US-09-815-048-3 9 US-09-954-531-560 10 US-09-770-444-621 10 US-09-770-149-538 9 US-10-161-510-9 9 US-10-161-510-8	10 US-09-822-849A-313 12 US-10-078-929-105 10 US-09-925-301-22 9 US-09-954-821-624 10 US-09-964-824A-261
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ALIGNMENTS

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Sequence 4. Application US/09935464
; Publication No. US20030027153A1
; GENERAL INFORMATION:
; APPLICANT: Meyer: Joanne
; APPLICANT: Barrington-Martin, Rory
; TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
; FILE REFERENCE: 3322/14702 US1
; CURRENT APPLICATION NUMBER: US/09/935,464
; CURRENT FILING DATE: 2001-08-23
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 1738
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                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-935-464-4
US-09-935-464-4
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RESULT 2
US-09-935-464-2

Sequence 2, Application US/09935464

Publication No. US20030027153A1

GENERAL INFORMATION:
APPLICANT: Mayer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYC,
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/14702 US1
CURRENT APPLICATION NUMBER: US/09/935,464

CURRENT FILING DATE: 2001-01-09

PRIOR PAPPLICATION NUMBER: US 09/757,300

PRIOR PLING DATE: 2001-01-09

NUMBER OF SEQ ID NOS: 90

SOFTWARE: Patentin Version 3.0

SEQ ID NO 2

SEQ ID NO 2
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Pred. No. 0;
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Best Local Similarity 99.9%;
Matches 1339; Conservative
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ORGANISM: Homo sapiens
US-09-935-464-2
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LENGTH: 157875
TYPE: DNA
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                   RESULT 3
US-09-935-464-1
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     GTGACCCTGGAGGACATCTATGAGAGCACCACCCACTACTACCTGGTCATGCAGCTTGTT
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APPLICANT Meyer, Joanne
APPLICANT Meyer, Joanne
APPLICANT Barrington-Martin, Rory
APPLICANT: Barrer, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSY
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 322/141702 USJ
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR PELLOR CONTROL OF SEQ. 10 NOS: 90
SOFTWARE: PATENTIN OF SEQ. 10 NOS: 90
SOFTWARE: PATENTIN VERSION 3.0
SEQ. ID NO ID NOS: 90
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Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.9%; Scc.
100.0%; Pre
                                                                                            Sequence 1, Application US/09935464 Publication No. US20030027153A1 GENERAL INFORMATION:
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DIAGNOSING AND TREATING NEUROPSYC
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Pred. No. 4e-212;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                             APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOS;
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REPERENCE: 3322/1H702 US.
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
                                                                                                                                    ATGGCATCGTCCACAGAGACTTAAAGCCCGGAAAACCTGCTTT 520
                                                                                                                                                                                                                               Sequence 7, Application US/09935464; Publication No. US20030027153A1; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIR
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT APPLICATION NUMBER: US/09/757,300
PRIOR PAPLICATION NUMBER: 2001-09
NUMBER OF SEQ ID NOS: 90
SOFTHARE: Patentin version 3.0
SEQ ID NO 46
LENGTH: 480
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                                      119 CCAACATCCGGAAAACCTTCATTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 CTCTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAACAGACCA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 CCAACATCCGGAAAACCTTCATTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAG 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 CACCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGATGCTGTGTGTTGAAAAAGATCAAGC
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                                                                                    TGGAGTTAACCTTGGAAGTTGACTATTTTAATGTCTGCCAGGAGTTCTAATCCTGCCTCT
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100.0%; Pred. No. 4.7e-218;
Live 0; Mismatches 0;
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Matches 462; Conservative
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OTHER INFORMATION: n=a or
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ORGANISM: Homo sapiens
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| Db 148396 CTA 148398
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Sequence 47. Application US/09935464

| Sequence 47. Application US/09935464
| Publication No. US20030027153A1
| GENERAL INFORMATION:
| APPLICANT: Meyer, Joanne
| APPLICANT: Barrington-Martin, Rory
| APPLICANT: Barrington-Martin, Rory
| APPLICANT: Barrington-Martin, Rory
| TITLE OF INVENTION: MISONDERS SUCH AS SCHIZOPHRENIA
| TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
| TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
| TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
| TITLE OF INVENTION: US/09/935,464
| CURRENT APPLICATION NUMBER: US/09/935,464
| CURRENT FILING DATE: 2001-08-23
| PRIOR FILING DATE: 2001-01-09
| NUMBER OF SEQ ID NOS: 90
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 47
| LENGTH: 467
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                                                                                      DB 9; Le
3.7e-125;
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Pred. No. 1.6e-94;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 CCTGCCTTCCGGGACAGCAGCCTGGAGATGAGA 274
                                                                                     Query Match 11.2%; Score 274; DE Best Local Similarity 100.0%; Pred. No. 3.7 Matches 274; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: n=a or g or c or t/u US-09-935-464-47
               COTHER INFORMATION: n equals a,t,g, or US-09-764-868-189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.7%;
Best Local Similarity 99.4%;
Matches 312; Conservative (
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NAME/KEY: SITE
LOCATION: (59)
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US-09-935-464-47
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US-009-935-464-50

Sequence 50, Application US/09935464

Sequence 50, Application US/09935464

Sequence 50, Application US-0935464

Sequence 50, Application Word200027153A1

SERREAL INFORMATION:

APPLICANT: Meyer, Joanne

APPLICANT: Meyer, Joanne

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA

TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA

TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA

TITLE OF INVENTION: DISORDERS: US/09/935,464

CURRENT APPLICATION NUMBER: US/09/935,464

CURRENT PILING DATE: 2001-01-09

NUMBER OF SEQ ID NOS: 90

SOFTWARE: Patentin Version 3.0

SEQ ID NO 50
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 319; DB 9; L6
Pred. No. 2.1e-147;
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100.0%; Pred. No. ...
0; Mismatches
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481 GCCTGCCCATCTGCATGAATG 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-935-464-50
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ORGANISM: Homo sapiens
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Sequence 177, Application US/09731872

Patent No. US20020102604A1

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Dobert, Severin
TITLE OF INVERTION: FULL-LENTTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3.REG
CURRENT APPLICATION NUMBER: US/09/731,872
CURRENT PILLING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 2000-13-08
PRIOR FILING DATE: 2000-03-06
NUMBER: OS 60/187,470
SEQ ID NOS: 482
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2299 ITCTAATCCIGCCICIGITCCCTTTTCICCTTGAAAGICCAGCACACCATTCTTGICC 2358
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Best Local Similarity 100.0%; Pred. No. 3.4e-81;
Matches 185; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2419 ATGGACATATTTTCTCTAAAAAAAAA 2447
                                                                                                                                                                     NAME/KEY: misc_feature; OTHER INFORMATION: n=a or g or c or t/u US-09-935-464-49
  PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 3.0
SEQ ID NO 49
LENGTH: 356
                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: 65..1024
US-09-731-872-177
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                                                                                                                                                                                                                                                                          Sequence No. US20030027153A1

Sequence No. US20030027153A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Barrington-Martin, Rory
APPLICANT: Alexander
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 332/14/102 US1
CURRENT FILING DATE: 2001-08-23
PRIOR PILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 3.0
IENOTH: 470
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Publication No. US20030027153A1
GENERAL INFORMATION:
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
TITLE OF INVENTION: ALexander
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
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                                                              181 TGAAGTGCATCAAGAAGTCACCTGCCTTCCGGGACAGCAGCAGCTGNAGAATGAGATTGCTG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 TGCCTTCCGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCATGA 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: misc_feature
; OTHER INFORMATION: n=a or g or c or t/u
US-09-935-464-48
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                                                                                                                                                                     CCCACTACTACCTG 314
                                                                                                                                             341 CCCACTACTACCTG 354
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ORGANISM: Homo sapiens
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US-09-935-464-48
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US-09-935-464-49
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APPLICANT: Meyer, Joanne
APPLICANT: Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSY
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TENDER 1. APPLICATION US/09817181

Sequence 1, Application US/09817181

Sequence 1, Application US/09817181

Sequence 1, Application US/09817181

GENERAL INFORMATION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/817,181

CURRENT APPLICATION NUMBER: US/09/817,181

CURRENT FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                   PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-04
PRIOR PILING DATE: 2000-08-04
PRIOR PILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 CCCTACAGCAAGCTGTGATTGCTGGTCCAT 198
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US-09-935-464-45
Sequence 45, Application US/09935464
Publication No. US20030027153A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: unsure

) LOCATION: (20)

; CTHER INFORMATION: n=A,T,C or G

US-09-796-692-7777
                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (10)
OTHER INFORMATION: n=A,T,C or
NAME/KEY: unsure
LOCATION: (19)
OTHER INFORMATION: n=A,T,C or
  PRIOR FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32; Conservative
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FEATURE:
NAME/KEY: unsure
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APPLICANT: Algate, Paul A.

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY

TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES

FILE REFERENCE: 2077.001200

CURRENT APPLICATION NUMBER: 05/196,692

CURRENT FILING DATE: 2000-03-01

PRIOR PAPLICATION NUMBER: 60/190,479

PRIOR PPLICATION NUMBER: 60/200,545

PRIOR PAPLICATION NUMBER: 60/200,303

PRIOR PAPLICATION NUMBER: 60/200,709

PRIOR PAPLICATION NUMBER: 60/200,709

PRIOR PAPLICATION NUMBER: 60/200,709

PRIOR PAPLICATION NUMBER: 60/200,709

PRIOR PAPLICATION NUMBER: 60/200,909

PRIOR APPLICATION NUMBER: 60/200,004

PRIOR PAPLICATION NUMBER: 60/200,009

PRIOR PAPLICATION NUMBER: 60/200,009

PRIOR PAPLICATION NUMBER: 60/200,001

PRIOR APPLICATION NUMBER: 60/200,001

PRIOR APPLICATION NUMBER: 60/200,001

PRIOR APPLICATION NUMBER: 60/200,001
                                                                                                                                                                                                                                     APPLICANT: Meyer, Joanne
APPLICANT: Barrington Martin, Rory
APPLICANT: Barrington Martin, Rory
APPLICANT: Barrington Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/11020 2031
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-09
PRIOR FILING DATE: 2001-09
NUMBER OF SEQ ID NOS: 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature
; OTHER INFORMATION: n = a or g or c or t/u
US-09-935-464-6
1297 ATGGACATATTTTCTCTAAAAAAAAA 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7777, Application US/09796692 Publication No. US20020198362A1 GENERAL INFORMATION: APPLICANT: Gaiger, Alexander
                                                                                                                                  US-09-935-464-6
; Sequence 6, Application US/09935464
; Publication No. US20030027153A1
; GENERAL INFORMATION:
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Matches 80; Conservative
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| FILE REFERENCE: 3322/14702 US1
| CURRENT APPLICATION NUMBER: US/09/935,464
| CURRENT FILING DATE: 2001-08-23
| PRIOR PILING DATE: 2001-01-09
| PRIOR FILING DATE: 2001-01-09
| NUMBER OF SEQ ID NOS: 90
| SOCTWARE: Patentin version 3.0
| SEQ ID NO 45
| LENGTH: 27
| TYPE: DNA
| ORGANISM: Artificial Sequence
| FAATURE: PATORE | DNA Probe
| COTHER INFORMATION: DNA PROBE
| COTHER INFO
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March 14, 2003, 14:03:36 ; Search time 38 Seconds
   (without alignments)
   1669.139 Million cell updates/sec
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

15: 17: 17: 19: 20: 22: 23:

			Description	Human calmodulin k	Human polypentide	Human polypeptide	Human diagnostic a	Human kinase (PKIN	Human polypeptide	Human CaM kinase I	Human kinase (PKIN	Human polypeptide	Amino acid sequenc
SUMMARIES			ID	AAE22764	AAM41547	AAM39761	AAU19443	AAE11777	AAM41268	ABB08178	AAE11768	AAM39482	AAB84359
			DB	23	22	22	22	22	22	23	22	22	22
		Query	Length	476	497	267	298	355	355	355	357	385	385
	dР	Query	Match	100.0	100.0	99.5	55.0	49.6	49.6	49.6	49.6	49.6	49.6
			Score	2513	2513	2499.5	1382	1246	1246	1246	1246	1246	1246
		Result	No.		7	e	4	S	ø	7	8	6	10

Human protein kina Murine Dendritic C Amino acid sequenc Amino acid sequenc Calmodulin-depende Human protein kina Novel human death domain Disease associated Drosophila melanog Human death domain Human protein kina Human polypeptide, Human protein sequenc Human protein kina Human kinase (PKIN Novel human diagno Drosophila melanog Drosophila melanog Drosophila melanog	screening; protein kinase; arthritic synovium; CAMK-X1;
11 1241 49.4 357 22 AAB0055B 12 1231.5 49.0 356 22 AAB80055 13 1231.5 49.0 356 22 AAB80055 14 1145 45.6 389 21 AAY88793 15 1070 42.6 358 19 AAY80159 16 1039 41.3 343 22 AB088176 20 944.5 37.6 280 22 AB88176 21 747.5 29.7 501 22 AAB8176 22 747.5 29.7 501 22 AAB8178 24 745.5 29.7 501 22 AAB8187 25 745.5 29.7 501 22 AAB8188 26 745.5 29.7 501 22 AAB8188 27 745.5 29.7 501 22 AAB8188 28 745.5 29.7 501 22 AAB8188 29 733.5 29.7 470 22 AAB8188 29 733.5 29.7 470 22 AAB8188 20 745.5 29.7 470 22 AAB8188 21 650.5 29.7 470 22 AAB8188 22 745.5 29.7 470 22 AAB8188 23 643.5 29.6 424 18 AAW1844 24 550.5 25.9 424 18 AAW1844 25 625.5 24.9 766 23 AAR66161 26 625.5 24.9 766 23 AAR66161 27 625.5 24.9 766 23 AAR66161 28 625.5 24.9 766 23 AAR65503 29 615.5 24.9 766 23 AAR65503 20 611.5 24.3 600 22 AAB5503 21 611.5 24.3 600 22 AAB5503 22 AAB66555 23 9 493 22 AB665555 24 5 599.5 23.9 493 22 ABB66655	RESULT 1 AAE22764 ID AAE22764 ID AAE22764 ID AAE22764; XX AC AAE22764; XX AC AAE22764; XX DT 09-AUG-2002 (first entry) XX KW Human calmodulin kinase, CAMK-X1. XX KW Human; cytostatic; antisense gene therapy; sc KW cancer; liver; colon; tumour; inflammation; a XX KW cancer; liver; colon; tumour; inflammation; a XX KW MC200224947-A2. XX BOMO sapiens. XX XX CS-SEP-2001; 2001W0-1B02237. XX PR 20-SEP-2001; 2001W0-1B02237. XX PR 20-SEP-2000; 20000S-23495P. PR 02-CCT-2000; 20000S-234558P. PR 02-CCT-2000; 2000US-234558P. PR 10-MAX-2001; 2001US-290555P. XX

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Wang
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                                                                                                                                         that modulates cancer associated protein kinase function. The invention also relates to a method for diagnosing cancer comprising determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase. The method is useful for diagnosing cancer. A protein kinase is besful for screening biological agents that modulate cancer associated protein kinase function. Downregulating the activity of protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon cancer. A nucleic acid encoding protein kinase is useful to screen biopsy derived tumours and inflammatory samples such as arthritic synovium, for amplified DNA in the cell or increased expression of corresponding mRNA or protein and is also useful to detect differences in expression levels such as molecular weight, amino acid and nuclectide sequences between the two cells. The present sequence is human calmodulin kinase, CAMK-XI.
                                                                                                                              The invention relates to a method for screening biologically active agent
                                          comprises determining the upregulation of expression sequence encoding a protein kinase or upregulation of
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Pred. No. 4.8e-220;
; Mismatches 0; Indels 0;
                                                      of a nucleic acid sequence encoding a protein ki
expression of the protein kinase, in the cancer
                                                                                                Claim 1; Page 64-65; 87pp; English.
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100.0%;
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Matches 476; Conservative
2002-394145/42.
                                            Diagnosing cancer,
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             N-PSDB; AAD36140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification.
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Zhang J;
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100.0%; Pred. No. 5.1e-220;
ive 0; Mismatches 0;
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Drmanac RT;
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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2000US-0552317.
2000US-0598042.
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13-NG-2000; 2000US-065450.
14-SEP-2000; 2000US-065191.
19-CCT-2000; 2000US-0639336.
29-NOV-2000; 2000US-0727344.
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Matches 476; Conservative
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09-JUL-2000;
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                                                                                                                                                                                                                                                                     Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; hamenostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for treating disorders
GTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFES
                                          PFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFA
                                                                    KSKWRQAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPV
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Zhang
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Yang Y,
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Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, us such as central nervous system injuries
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                                                                                                                                                                                                                                                      polypeptide SEQ ID NO 2906.
                                                                                                                                                                                                  AAM39761 standard; Protein; 567
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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2000US-0552317.
2000US-0598042.
2000US-0653450.
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09-JUL-2000;
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               system, such as peripheral nervous injuries, peripheral neuropathy and localized neuropaths and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, hemotactic/chemokinetic activity, hemosatatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and Note: The sequence data for this patent did not form part of the printed
peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; receptor; diagnostic; therapeutic; gene therapy; vaccine; cell proliferative disorder; Crohn's disease; lymphoma; leukaemia; acquired immune deficiency syndrome; AIDS; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                  1 MGRKEEDDCSSWKKOTTNIRKTFIFMEVLGSGAFSEVFLVKORLFGKLFALKCIKKSPAF
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                                                                                                                                                                                                                                                                                                     567;
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be used to treat diseases of the
                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                   Score 2499.5; DB 2 Pred. No. 1.1e-218;
                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                   99.58;
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                                                                                                                                                                                                                                                                                                                                            Matches 476; Conservative
the invention may
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                                                                                                                                                                                                                                                            567 AA;
                                                                                                                                                                                                                       specification.
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AAE11777 standard; Protein; 355
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                                                                                                                                    55.0%;
99.3%;
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                                                                                                                                                             Matches 265; Conservative
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                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the invention relates to polynucleotides (I) encoding diagnostic and therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and proteins involved in growth and development and receptors. (I) and proteins involved in the prevention, diagnosis and treatment of diseases associated with inappropriate DITHP expression. For example, (I) and corporated disorders associated with decreased polypeptide expression by rectifying mutations or deletions in a patient's genome, that affect the activity of the DITHPS, by expressing inactive proteins or supplementing the patient's own production of them. (I) and (II) may be used to treat diseases, for example, cell proliferative disorder, crohn's diseases, acquired immune deficiency syndrome (AIDS). Immphoma, leukaemia, autoimmune disorders, and respiratory disorders. Additionally, (I) may be used to produce the DITHPS, by inserting the nucleic acids in the complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones AL;
, Daffo A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chan Chen A, D'Sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE; Dufour GE, Flores V, Fong WT, Greenawalt LB, Hillman JL, Liu TF, Roseberry AM, Rosen BH, Russo FD, Stockdreher TK, Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W, Hodgson DM, Lincoln SE, Jackson S;
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2000US-0185216.
2000US-0203785.
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2000US-0204525.
2000US-0204821.
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2000US-0205232.
2000US-0204815.
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2000US-0184771.
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2000US-0184837.
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2000US-0205285
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WO200162927-A2.
                                                                                        24 - FEB - 2000;
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16-MAY-2000;
16-MAY-2000;
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24-FEB-2000;
24-FEB-2000;
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17-MAY-2000;
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24-FEB-2000;
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samples, and therefore which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies against DITHPs and in assays to identify modulators of DITHP expression and activity. The anti-DITHP antibodies and antaqonists may also be used to down regulate expression and activity. The anti-DITHP antibodies may also be used as diagnostic agents for detecting the presence of DITHPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). Adul9415-Adul9625 represent human diagnostic and therapeutic (DITHP) polypeptides of the invention.
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                                                                                                                                                                                                                                                                                                                                                                            Length 298;
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/note= "Tyrosine Kinase catalytic domain"
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te= "Tyrosine kinase catalytic domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                        Score 1382; DB 22;
Pred. No. 2.9e-117;
0; Mismatches 2;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for preventing diagnosing and immune disorders -
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                                                                                                                                                                                                                                                                                                                                                                                        Yao MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention relates to human kinases (PKIN) and the nucleic
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Bandman O, Lu DAM, Lal P, Burford N, Khan FA, Walia NK, Yac
Patterson C, Burrill JD, Marcus GA, Zingler KA, Recipon SA,
Policky JL, Thornton M, Tang YT, Hafalia A, Ellott VS, Baug
Walsh RT, Ramkumar J, Borowsky ML, Au-young J, Hillman JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human kinases and nucleic acids, us treating cancers, inflammation and
                                                                                                                           2000US-200226P.
2000US-202339P.
2000US-203505P.
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2000US-207739P.
2000US-208795P.
                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS INC.
                                                20-APR-2001; 2001WO-US12992
                                                                                                      2000US-199021P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 73.1 nes 237; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAD18826
                                                                                                                           28-APR-2000;
05-MAY-2000;
11-MAY-2000;
                                                                                                                                                                                                       18-MAY-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                          01-JUN-2000;
                                                                                                   20-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gururajan R;
01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein.
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Matches
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the encoded polypeptides (AAAA3213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Perkinson's disease, Hutington's disease, amyotrophic utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang D;
                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN 298
                241 DSPYNDDISDSAKDFIRNLMEKDPNKRYTCEQAARHPWIAGDTALNKNIHESVSAQIRKN 300
                                                                                                                                                                                                                                                                                                                       peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; Hamenstatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ren F, War Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen R, Ma Y,
Xu C, Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; SEQ ID NO 6199; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acids and polypeptides,
                                                                                                                                                                           A.
                                                              FAKSKWRQAFNAAAVVHHMRKLHM 322
                                                                                301 FAKSKWRQAFNATAVVRHMRKLHL 324
                                                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 6199.
                                                                                                                                                                           standard; Protein; 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-063312.
2000US-0653450.
2000US-065191.
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0693036.
2000US-0727344.
                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAI60424
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355 AA;
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28-APR-2000;
05-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
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                                                                                                                                                                                                                                                                                                                         AAE11768;
           Sequence
                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                            Matches
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                                                                                                         61 GKESSIENEIAVLAKIKHENIVALEDIYESPNHLYLVMQLVSGGELFDRIVEKGFYTEKD 120
                                                                                                                                   178
                                                                                                                                           238
                                                                                                119
                                                                                                                                                                                                        ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN 298
                                                                                                                                                                                                                 Gaps
                                                                      1 MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPA 59
                                                                                              60 FRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKD
                                                                                                                                   ASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEONG-IMST
                                                                                                                                                                     ACGIPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEF
                                                                                                                                                                               Novel polypeptide human CaM kinase I 39.05 and polynucleotide for encoding said polypeptide –
                                                                                                                                                                                                                                                                                                                                                                          Human; CaM kinase I 39.05; nervous disease; arrhythmia; tumour;
                                            ;;
                          Length 355;
                                            Indels
                          ; Score 1246; DB 22;
; Pred. No. 9.4e-105;
40; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 27-28 (disclosure); 35pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                         Human Cam kinase I 39.05 polypeptide.
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                                                                                                                                                                                                                                          FAKSKWRQAFNAAAVVHHMRKLHM 322
                                                                                                                                                                                                                                                    ABB08178 standard; Protein; 355
                          49.68;
73.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000; 2000CN-0119405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000; .2000CN-0119405
                                                                                                                                                                                                                                                                                                                                       23-SEP-2002 (first entry)
                                  al Similarity 73.13
237; Conservative
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N-PSDB; ABL60905.
         A.
         355
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                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    CN1333357-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2002.
                                                                                                                                                                                                                                                                                                                       ABB08178;
        Sequence
                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                     enzyme.
                                           Matches
                                                                                                                                  120
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ABB08178
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                                                                                                                                                                                                                                                61 GKESSIENEIAVLRKIKHENIVALEDIYESPNHLYLVWQLVSGGELFDRIVEKGFYTEKD 120
                                                                                                                                                                                                                                                                                                                           ASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMST 178
                                                                                                                                                                                                                                                                                                                                                       FRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN 298
                                                     Gaps
                                                                                                          1 MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPA 59
                                                                                                                                        ACGTPGYVAPEVLAQKPYSKAVDCWS1GV1TY1LLCGYPPFYEETESKLFEK1KEGYYEF
                                                       2;
Length 355;
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41..357
/label= Human_mature_PKIN-2_protein
                                                       Indels
; Score 1246; DB 23;
; Pred. No. 9.4e-105;
40; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Protein kinase domain"
23..279
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24..270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE11768 standard; Protein; 357 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAKSKWRQAFNAAAVVHHMRKLHM 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human kinase (PKIN)-2 protein.
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2000US-200226P.
2000US-202339P.
     49.68;
                           al Similarity 73.1%;
237; Conservative
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2000US-203505P. 2000US-205564P.

18-MAY-2000;

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AAM39482 standard; Protein; 385 AA.
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2000US-055317.
2000US-0598042.
2000US-0620312.
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2000US-0662191.
2000US-0693036.
2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-2000; 2000WO-US34263.
                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 237; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C, A
Wang Z, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385 AA;
                                                                                                                                                                                   nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                            WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-NOV-2000;
                                                                                                          22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                26-JUL-2001
                                                                                                                                                                                                                                                                         leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT,
                                                                          AAM39482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang .
Zhao (
                      AAM39482
   RESULT
                                                                        The present invention relates to numen kinases (FALM) and the nucleic used in the prevention, diagnosis and treatment of diseases cancers, adenocarcinoma, leukaemia, sarcoma, immune disorder, Addison's disease, adenocarcinoma, leukaemia, sarcoma, immune disorder, Addison's disease, adenocarcinoma, leukaemia, sarcoma, immune disorder, Addison's disease, cquir, microbial infections, cardiovascular disease and/or inflammation, mysthenia gravis, atherosclerosis, cirrhosis, osteoporosis, myocardial infarction, cataract, grower's disease, inpid disorder, iseizure disorder, pulmonary embolism, Gaucher's disease, renal disease and obesity. PKIN may be used to treat disorders associated with decreased PKIN expression by rectifying mutations or deletions in a patient's genome that affect the activity of PKIN by expressing inactive proteins or to supplement the patients own production of PKIN PKIN moleic acids may be used to produce the PKIN polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. PKIN nucleic acids and its complementary sequences may also be used as DNA probes in nucleic assays to detect and quantitate the presence of similar nucleic acid sequences in samples and therefore which patients may be in the protein and its complementary sequences may also be used as DNA probes in canded acid sequences in samples and therefore which patients may be in a protein.
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                                                                                  i AR, Tribouley CM, Kearney L, Griffin JA, Nguyen DB, U DAM, Lal P, Burford N, Khan FA, Walia NK, Yao MG; Burrill JD, Marcus GA, Zingler KA, Recipon SA, Lu Y; Thornton M, Tang YT, Hafalia A, Elliott VS, Baughn MR; mkumar J, Borowsky ML, Au-young J, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human kinases and nucleic acids, useful for preventing diagnosing and treating cancers, inflammation and immune disorders -
                                                                                                                                                                                                                                                                                                                                                             The present invention relates to human kinases (PKIN) and the nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 FRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 ASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQ1QKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.6%; Score 1246; DB 22; 73.1%; Pred. No. 9.5e-105; tive 40; Mismatches 45;
                                                                                                                                                                                                                                                                                                                         Claim 1; Page 124-125; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAKSKWRQAFNAAAVVHHMRKLHM 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000; 2000US-207739P. 01-JUN-2000; 2000US-208795P.
                                                      (INCY-) INCYTE GENOMICS INC.
                                                                                               Bandman O, Lu Lor.,
Patterson C, Burrill JD,
Thornton M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 49.6
Best Local Similarity 73.1
Matches 237; Conservative
                                                                                                                                                            Ramkumar J,
                                                                                                                                                                                                                 2001-611740/70.
                                                                                       Gandhi AR,
O, Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 AA;
                                                                                                                                                                                                                                  N-PSDB; AAD18817
                                                                                                                                                                             Gururajan R;
                                                                                                                                          Policky JL,
Walsh RT, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                      peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehmer's; Parkinson's disease; hauntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ren F, Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.6%; Score 1246; DB 22; 73.1%; Pred. No. 1.1e-104; Live 40; Mismatches 45;
                                                                                     cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asundi V, Chen R, Ma Y,
Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO 2627; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assays for receptor activity, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     such as central nervous system injuries
                                                                                         immunosuppressant;
Human polypeptide SEQ ID NO 2627.
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us-09-960-643-2.rag

385 AA;

Sequence

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The present sequence represents a kinase polypeptide. The kinase polynucleotides and polypeptides are useful in therapeutic, diagnostic and planmacogenic applications. They are useful for the detection of mutant kinases, or inappropriately expressed kinases for the diagnosis of a disease or disorder. They are useful for screening for drugs (or high throughput screening of combinatorial libraries) effective in the treatment of symptomatic or phenotypic manifestations of that disease or disorder. The polynucleotide sequence is useful as a source of probes and primers, which can be used to screen libraries, isolate clones, and prepare cloning and sequencing templates.
                                                                                                                                                                                         240
                                                                                                             178
                                                      119
                                                                   61 GKESSIENEIAVLRKIKHENIVALEDIYESPNHLYLVWQLVSGGELFDRIVEKGFYTEKD 120
                                                                                                                         Novel isolated human kinase polynucleotide that shares structural similarity with animal kinases including calcium/calmodulin-dependent protein kinases and serine/threonine protein kinases, useful in
FRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKD
                                                                                                                                                                                ASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMST
                                                                                                                                                                ACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEF
                                                                                                                                                                                                                      ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zambrowicz
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a human kinase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Friedrich G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; kinase; human disease; human disorder.
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                                                                                                                                                                                                                                                                                        FAKSKWRQAFNAAAVVHHMRKLHM 322
                                                                                                                                                                                                                                                                                                                                                                  AAB84359 standard; Protein; 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LEXI-) LEXICON GENETICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-381667/40.
N-PSDB; AAH25118.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 numan; protein kinase; PTK; STK; cancer; cardiovascular disease;
metabolic disorder; immune related disease; neurological disorder;
neurodegenerative disorder; inflammatory disorder; infectious disease;
reproductive disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polynucleotides
                                                                                                60 FRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKD 119
                                                                                                              ASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMST 178
                                                                                                                                                                                                                                            ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN 298
                                                                                                                                                                                                                                                         Gaps
                                                 1 MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPA 59
                                                              ACGIPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEF
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  Length
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             1.1e-104
  ВВ
                          Mismatches
 Score 1246;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                            322
                                                                                                                                                                                                                                                                                                       Claim 7; Figure 2; 433pp; English
                      40;
                                                                                                                                                                                                                                                                                                                                                                            AAU03508 standard; Protein; 357
                                                                                                                                                                                                                                                                                            FAKSKWRQAFNAAAVVHHMRKLHM
49.68;
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                          Conservative
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Clary D;
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             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-2001
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                         Matches 237;
                                                                                                                                                                                                                                                                                                                                                                                                    AAU03508;
 Query Match
               Local
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07-DEC-2000; 2000WO-US33240.
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                        N-PSDB; AAC90432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; kinase;
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                                                                                                                                                                                                    Sequence
                                                                                                                                                                                 family.
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prevention, diagnosis and the polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with langpropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoletic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. parkinson's disease), inflammatory disorders (e.g. asthma), infectious disease (e.g. HVV) and reproductive disorders (e.g. infertility). Used for gene therapy and as DNA probes in diagnostic assays. The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify
                                                                                                                                                                                                                                                                                                                                                          FRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKD 119
                                                                                                                                                                                                                                                                                                                                                                                       239 ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLOIQKN 298
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                 Murine; Dendritic Cell Kinase; MDCK-3; autoimmune disorder; allergy; wound healing; periodontal disease; inflammatory disease; tumour; infection; Ca2+/calmodulin-dependent kinase family.
                                                                                                                                                                                                                     MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPA
                                                                                                                                                                                                                                                                                                      ASLVIQOVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMST
                                                                                                                                                                                                                                                                                                                                               ACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEF
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                                                                                                                                                                               Length 357;
                                                                                                                                                                                                   Indels
                                                                                                                                      modulators of protein kinase expression and activity.
                                                                                                                                                                              Score 1241; DB 22;
Pred. No. 2.7e-104;
40; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB50055 standard; Protein; 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine Dendritic Cell Kinase 3.
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                                                                                                                                                                               49.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                 Matches 236;
                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB50055;
                                                                                                                                                                              Query Match
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AAB50055
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Novel murine and human kinase nucleic acids useful for treating inflammations, infections, tumors, allergies, autoimmune diseases, and for stimulating or suppressing immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GKESSIENEIAVLRKIKHENIVALEDIYESPNHLYLVMQLVSGGELFDRIVEKGFYTEKD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 49.1%; Score 1233; DB 22; Best Local Similarity 72.5%; Pred. No. 1.4e-103; Matches 235; Conservative 40; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of a human kinase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Ala encoded by GCTGGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human disease; human disorder.
                                                                                                                            Claim 10; Page 92-94; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAKSKWRQAFNAAAVVHHMRKLHM 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 FAKSKWRQAFNATAVVRHMRRLQL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 AA;
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Homo sapiens
                                                                       Domain
                                                                                                                                                                         Domain
                                                                                                                                                                                                               Region
   3;
                                                                                                                                                                             The present sequence represents a kinase polypeptide. The kinase polymoral confides and polypeptides are useful in therapeutic, diagnostic and pharmacogentc applications. They are useful for the detection of mutant kinases, or inappropriately expressed kinases for the diagnosis of a disease or disorder. They are useful for screening for drugs (or high throughput screening of combinatorial libraries) effective in the treatment of symptomatic or phenotypic manifestations of that disease or disorder. The polymucleotide sequence is useful as a source of probes and primers, which can be used to screen libraries, isolate clones, and prepare cloning and sequencing templates.
                                                                                                          Novel isolated human kinase polynucleotide that shares structural similarity with animal kinases including calcium/calmodulin-dependent protein kinases and serine/threonine protein kinases, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                    178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238
                                                                                                                                                                                                                                                                                                                                                                                                       61 GKESSIENEIAVLAKIKHENIVALEDIYESPNHLYLVMQLVSGGELFDRIVEKGFYTEKD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                               ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKD 119
                                                                                                                                                                                                                                                                                                                                                                       MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKATGKLFAVKCIPKKALK 60
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                     MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                   ASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a human phosphorylation effector PHSP-25.
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                                                                                                                                                                                                                                                                                                            49.0%; Score 1231.5; DB 22; Length 356; 72.8%; Pred. No. 2e-103; Live 40; Mismatches 45; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphorylation effector; PHSP; proliferative disorder; disorder; neuronal disorder.
                                                  Zambrowicz
                                                 Friedrich G,
                                                  Turner CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY68793 standard; Protein; 389 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAKSKWRQAFNAAAVVHHMRKLHM 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 31; 32pp; English.
                             (LEXI-) LEXICON GENETICS INC
         99US-0169428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 72.89
Matches 236; Conservative
                                                 Scoville J,
                                                                             WPI; 2001-381667/40.
N-PSDB; AAH25119.
                                                           Sands AT;
                                                                                                                                                                                                                                                                                          356 AA;
                                                                                                                                        therapeutics
         07-DEC-1999;
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                                                 Donoho G,
                                                           Abuin A,
                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
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AAY68769-95 and AAY68797-99 represent human phosphorylation effectors (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT, Corley NC, Guegler KJ, Baughn MR;
n O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;
                                                                            'note= "potential phosphorylation site"
                                                                                                                                                                                                     'note= "potential phosphorylation site"
                                    'note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                     site"
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375
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                                                                                                                                                                                                                                                                                                                                                                                  172..184
/note= "STK core catalytic motif"
                                                                                                                     'note= "protein kinase catalytic
                                                                                                                                                                                                                                                                                                     152..208
/note= "PTK core domain"
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  Location/Qualifiers
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98US-0173482
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DAM, Shih LL;
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N-PSDB; AAZ46162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JAN-1999
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12-JAN-1999
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given in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated
                                                                                                                                                                                                    NEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQ 126
                                                                                                                                                                                                              127 VLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMSTACGTPGY 185
                                                                                                                                       Gaps
                                                                                                                                                           99
                                                                                                                                                                       246 ISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWR
                                                                                                                                                                                                                                                                                                                                          KKQTTNIR--KTFI---FMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLE
                                                                                                                                                                                                                                                                                      186 VAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDD
                                                                                                                                       8;
                                                                                                                 45.6%; Score 1145; DB 21; Length 389; ilarity 71.0%; Pred. No. 1.7e-95; Conservative 39; Mismatches 45; Indels 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat; calmodulin-dependent protein kinase; clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Foye PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calmodulin-dependent protein kinase clone 29.
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Sutcliffe JG;
                                                                          with increased PHSP expression/activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "encoded by TG"
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Misc-difference 344
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, Kilduff TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-145352/13.
N-PSDB; AAV18867.
                                                                                                                            Similarity
                                                                                               389 AA;
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Gautvik VT,
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Matches
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AAW50159
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251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                        13 KKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIAV 71
Nucleic acid encoding hypocretin of rat and mouse - useful for diagnosis and treatment of neurological disease, homeostatic dysfunction etc., also sequence for calmodulin kinase-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 KYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAA
                                                                                                                                                                                                                                                                                                                192 AQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAK
                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFLRHIRKL-----GOSPEGE----EASROGMTRHSHPGLGTSQSP 341
                                                                                                                                                                                                                                                    Indels
                                                                                                                   The present sequence is rat calmodulin-dependent protein
                                                                                                                                                                                                              Score 1070; DB 19;
Pred. No. 1e-88;
5; Mismatches 74;
                                                                                                                                                                                                                                                    55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: March 14, 2003, 14:08:36
                                                                               English
                                                                                                                                                                                                                42.6%;
                                                                               Disclosure; Fig 6; 111pp;
                                                                                                                                                                                                                                                          207; Conservative
                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                            358 AA;
                                                                                                                                         kinase clone 29
                                                                                                                                                                              Seguence
                                                                                                                                                                                                                  Query Match
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Database :

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

I (base 1 to 1126)

National Institutes of Health, Mammalian Gene Collection (MGC)

In (published (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Invitrogen
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Invitrogen
Contact: Arrayed by: The 1.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://mage.llnl.gov

Plate: LLAM12713 row: 1 column: 19

High quality sequence stop: 623.

Incation/Qualifiers
        BI818261 603032510
BI772626 603060879
BM921532 AGENCOURT
BQ102407 1121-007.x
BG715920 602676657
ALI34342 DEKEZB470
AW016039 UI-H-BIDP
AA838372 of29a11.s
BQ086330 1121-07.y
BI834635 603399418
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BI667965 603392877
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BG170935 G023912312
RO5661 Yf87d09.rl
BG293660 G02390529
BC934044 AGENCOURT
BP950790 RC3-NN019
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AN713924 UI-R-ACI-
AW521224 UI-R-B00-
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AW25124 UI-R-B00-
AW25124 UI-R-B01-
AW251240 UI-R-B01-
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AW12501 UI-R-B13-
AW321699 UI-R-B00-
BE944047 UI-R-BH3-
AW492153 UI-R-B00-
BE99348 G23103 MA-
BB71015 BB871015 BB87
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BI084101 602869466
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BI084897 602869466
                                                                             March 14, 2003, 17:23:21 ; Search time 3882 Seconds
(without alignments)
10208.747 Million cell updates/sec
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           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                          /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: Not1; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
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/clone="IMAGE:5724450"
/clone_lib="NHH_MGC_125"
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/ Organism="Homo sapiens"
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/ Clone=TriAAGE:517936"
/ Clone=TriAAGE:51796
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60308366F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5179336 5',
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAMILY row: c column: 17
High quality sequence stop: 808.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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ilarity 100.0%; Pred. No. 5.1e-306;
Conservative 0; Mismatches 0;
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us-09-960-643-1.oli.rst

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                                                                                                                                                                                                                                                                                                                                                                                                     BI824483 · 740 bp mRNA linear EST 04-OCT-2001 603038855F1 NIH_MGC_115 Homo saplens CDNA clone IMAGE:5179957 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                    TCTAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGGCATCATGTCC
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CCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCAT
                                                                CAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAG
                                                                                                          AAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAGAAT
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/db_xref="taxon:9606"
/clone="IMAGE:5179957"
/clone_lib="NIH_MGC_115"
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BI824483.1 GI:15936033
                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
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1048 bp mRNA linear EST 20-JUN-2001
Homo sapiens cDNA clone IMAGE:5013856 5',
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male lung, age 27; and 1 male testis, age 69. Library i oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                1 TGGAGTGGGAGCTCAAGCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAACT
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                                                                                                                                                    Length 740;
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Best Local Similarity 100.0%; Pred. No. 2.2e-284;
Matches 710; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
/db_xxef="taxon:9606"
/db_xxef="taxon:9606"
/clone="IMAGE=5013856"
/clone=lib="NIH_MGC_102"
/tissue_type="*epidermoid carcinoma, cell line"
/lab_host="Blu108 (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAho! sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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                                                                                                             L motional institutes of nearth, mammatain dens collection (mot) Contact: Robert Strausberg, Ph.D.
Email: ogapbs-remail.nih.gov
Tissue procurement: ArCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Caboratories, Inc.
cDNA Library Preparation: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://amage.lln.gov
Plate: LLCM1820 row: d column: 17
High quality sequence stop: 853.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1048)
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                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 1.2e-273;
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28.0%; Score 684; DB
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 684; Conservative 0; Mismatches
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/db_xref="taxon:9606"
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/clone="IxAGE:732298"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="Alph08"
/note="Organ: brain; Vector: pcMV-SPORT6; Site_l: EcoRV (destroyed); Site_l: Not1; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library sonstructed and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
87 a 308 c 294 g 240 t
                                                                                                                                                                                                                                                                                                                                                                 BM807335 1129 bp mRNA linear EST 05-MAR-2002 AGENCOURT_6575096 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732298
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                            GACAGGCAGCTCCCCAIGGTGGTCTGCCTGTGAGCTCTTCAAGTTCTAATCCTTAACTCC 2084
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
to column: 19
High quality sequence start: 11
High quality sequence stop: 651.
Location/Qualifiers
CTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAACAGACCACC 120
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
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                                                                            AACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT
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                                                                                                                                                        CAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAG
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High quality sequence stop: 832.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/db_xref="taxon:9606"
/clone="ntwaGE:5013856"
/clone="ntwaGE:5013856"
/clone="ntwaGE:5013856"
/tissue_type="epidermoid carcinoma, cell line"
/tissue_type="epidermoid carcinoma, cell line"
/lab.host="DH108 (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTBP; Site_1: XhoI;
Site_2: EcoRi; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAhoI sites using the
following 5' adaptor: GGACGGG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
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                                                                                                                                 /note="Organ: Drain; Vector: pCNV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber full-length. Research Genetics tracking code 019. Note: this is a NIH,MGC Library."
                           BI753035 731 bp mRNA linear EST 25-SEP-2001
603025844F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5196323 5',
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100.0%; Pred. No. 1.9e-259;
ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11011 row: g column: 12
High quality sequence stop: 729.
Location/Qualifiers
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                                                       mRNA sequence.
BI753035
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RESULT 7
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BIB18261 742 bp mRNA linear EST 04-OCT-2001
603032510F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5173587 5',
mRNA sequence.
BIB18261
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pcMV-SPORT6; Site_1: NotI: Site_2: ECORV (destroyed); RNA
source anonymous pool of G male brains, age range 23-7; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (ECORV site is
destroyed upon cloning). Average insert size 1: 8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammallan Gene Collection (MGC)
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAMIA32 row: d column: 04
High quality sequence stop: 742.
Location/Qualifiers
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                          CTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAGAATGGCATCGTCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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Pred. No. 1.2e-253;
0; Mismatches 1;
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/lab_host="DH10B"
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/clone="IMAGE:5173587"
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NIH MGC http://mgc.nci.nih.gov/.
NIH MGC http://mgc.nci.nih.gov/.
Dupublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                       TCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTTTTCCTGGTGAAGCAAA
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                                                                                                                              GACTGACTGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCACCTGCCTTCCGGGACA
                                                                                                                                                                        GCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCATGAAAACATTGTGACCC
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BI772626
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VERSION
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TITLE
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/note—"Organ: pooled lung and spleen; vector: pcWV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 44 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NILMG Library."
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                      20
                           column:
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/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
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/organism="Homo sapiens"
                                          High quality sequence start: 2
High quality sequence stop: 808
Location/Qualifiers
                                                                                                                                                             /db_xref="taxon:9606"
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http://image.llnl.gov
Plate: LLAM11527 row: m
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614 AC 615
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutherla: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1068)

National Institutes of Health, Mammallan Gene Collection (MGC)

National Institutes of Health, Mammallan Gene Collection (MGC)

National Institutes of Health, Mammallan Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov.

Plate: LLAM12788 row: b column: 19

High quality sequence stops: 592.

Location/Qualifiers

J. ..1068

J. ..1068
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pcMv-SPORT6; Site_1: Not1; Site_2: EcoRv (destroyed); RNA
source annonymous pool of 6 male brains, age fange 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRv site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MCC Library."

281 c 260 g 248 t
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                BM921532 12-MAR-2002
AGENCOURT_6708041 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5753010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:5753010"
/clone_lib="NHH_MGC_ll5"
/lab_host="DH10B"
                                                        5', mRNA sequence.
BM921532
BM921532.1 GI:19371911
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Matches 601; Conservative
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E Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (Dases 1 to 479)

S Lemishka, I., Scearce, M., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Pape, D., Wylie, T., Marrin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McZenn, R., Cole, R., Tsägareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium

L Unpublished (2000)

Other_ESTS: ij2lc07, yl

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium

Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOLUGAU7 479 bp mRNA linear EST 29-APR-2002 ij21c07.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens EQNA clone IMAGE:6135181 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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Library was constructed by Dr. Douglas Melton DNA sequencing by:
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center This clone is
available royalty-free through LLNL; please contact the IMAGE
consortium (info@image.llnl.gov) for further information
Seq primer: -40UP from Gibco
High quality sequence stop: 448.

Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6135181"
/sex="Both"
                                                                                                                                                                                                                                               493
                                                                                                                                                                                                                                                                                                            540
                                                                                                                                                                              421 AAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAGAAT 480
                                                                                          314 GAAAACATTGTGACCCTGGAGGACATCTATGAGGACCACCACCACTACTACTGGTCATG
                                                             361 CAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAG
                                                                                                                                                                                                                                                                                                            GGCATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCTGAAGAGAAC
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/dev_stage="Adult"
/lab_host="DH10B"
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Tel: 617-495-1812
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fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Baall: gapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Stroshiyuki and Piero Carninoi (RIREN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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                                                                                                                                                                                                                          Length 479;
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100.0%; Pred. No. 2.5e-188;
ive 0; Mismatches 0;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                        library
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BG715920
BG715920.1 GI:
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pBluescript KS+); Site_1: BamHI; Site_2: Sall-XhoI (gtcgag pluescript KS+); Site_1: BamHI; Site_2: Sall-XhoI (gtcgag size-selected for average insert size 2: 3k b and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                               /note="Organ: brain; Vector: pBluescriptR (modified
   can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortlum/LLNL at: http://image.llnl.gov
Plate: LLAMJ0688 row: e column: 17
High quality sequence stop: 766.
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                                                                                                                                                                                                                                                                                                                                                                            Score 473; DB 12;
Pred. No. 6.6e-186;
0; Mismatches 3;
                                                                                                                                                                  /tissue_type="hypothalamus"
/lab_host="DH10B"
                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4799224"
/clone_lib="NIH_MGC_96"
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|larity 99.5%;
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623; Conserv
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemannédkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                     Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sl sequence also available.
This clone (DKEZp5470044) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANNY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1764
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DKFZp5470044_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone
DKFZp5470044 5', mRNA sequence.
                                                                                                                                                                                                                                                            ,S.
EST (Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1705 CGTAGAAGCCTTGTTGAAGCTGTGAGCAGAGAAGCGGTGCCCACCAGCTTCCAGGTCTC
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109 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DkFzp5470644"
/clone_lib="547 (synonym: hfbr1)"
/tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 450; DB 9; I
Pred. No. 2.8e-176;
0; Mismatches 1;
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154 c 132 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="fetal"
/lab_host="X1-2blue"
                                                                                                               AL134342.1 GI:6602529
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99.8%;
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                                                                                                                                                                                                                                                                                                           Unpublished (1999)
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KEYWORDS
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1...46 / Corganism="Homo sapiens"  
/db_xref="taxon:9606"  
/db_xref="taxon:9606"  
/db_xref="taxon:9606"  
/clone="Inba"NCI_CGAP_Sub2"  
/lab_host="DH10B (Life Technologies)"  
/lab_host="DH10B (Life Techn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution information can be found through the I.M.A.G.E. Consortium/Lill.at:
Www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW016039 484 bp mRNA linear EST 10-SEP-1999 UI-H-BIOp-abf-c-11-0-UI.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711445 3', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 484)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
GTGTCACCTTCTCCAAGCAAAGCCATATGGAGCATCTACCCAGACTCCCACTCTGCACAC 1944
                                                                                                                                                                                                                                            421 ACTCACCTCCACCTCTCAAGCCTCCAACCTCTTGGCCAGATTGGGCTCATTAATGTCGTT
                                         361 GIGTCACCTTCTCCAAGGAAAGCCATATGAGGAGCATCTACCAGACTCCCACTCTGCACA
                                                                                                                                                                                              ACTCACTCCCACCTCTCAAGCCTCCAACCTCTTGGCCAGATTGGGCTCATTAATGTCGTT
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NCI_CGAP_CO10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDS 1057416-1061255, 1144584-1145351) The resulting subtracted library contained 4 million recombinants.
Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.
TAG_LIB-NCI_CGAP_Brn26
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 410)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                   2013 ATCTGCATGAATGACAGGCAGCTCCCCATGGTGGTGTCTGCCTGTGAGCTCTTCAAGTTCTA 2072
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                                                                                                                                                                                                                                                                                                             Gaps
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Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert.Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                  Length 484;
                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                  Score 426; DB 10; I
; Pred. No. 2.6e-166;
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                     TAG_SEQ=ATAGG
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AA838372/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
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Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Stratagene, Inc. cDNA Library Preparation: Stratagene, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 944 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="kidney tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="Yorgan: kidney; Vector: Bluescript SK-; Site_1:
/note="Yorgan: kidney; Vector: Bluescript SK-; Site_1:
Oligo dr. Pooled kidney tumors. 5' adaptor sequence: 5'
GAATTGGGCACGAG 3' 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb.'
19 c 130 g 89 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.8%; Score 410; DB 9; Le
100.0%; Pred. No. 1.2e-159;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1422524"
/clone_lib="NCI_CGAP_Kid6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: March 15, 2003, 05:00:43 Job time : 3894 secs
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Patent No. 6222029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Dealert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
US-09-247-155-72
PCT-US94-10080-1
US-08-128-738-1
US-09-328-256-13
US-09-395-115-13
US-09-395-115-13
US-09-45-45-26-13
US-09-46-46-46-13
US-08-43-47-13
US-08-21-13-13
US-08-21-1934-55
US-08-21-1934-55
US-08-21-1934-55
US-08-21-1934-55
US-08-940-0868-55
US-08-940-0868-55
US-08-940-0858-55
US-08-940-0358-55
US-08-940-0358-55
US-08-940-0358-55
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US-08-940-0358-55
US-08-940-0358-55
US-08-940-0358-55
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LOCATION: 87..191

IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 5.6

OTHER INFORMATION: seq FIFMEVLGSGAFS/EV
US-08-905-223-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEE: Knobbe, Martens, Olson & Bear: 5.501 West Broadway
an Diego
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
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NAME: ISraelsen, Ned A.
REGISTRATION UNDRER: 29,655
REFERENCE/DOCKET UNDRER:
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo Sapiens
TISSUE TYPE: Brain
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      NUCLEIC ACID
EDNESS: DOUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
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CLASSIFICATION: 536
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         STRANDEDNESS:
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Sequence 8, Appli
Sequence 1, Appli
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Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 9, Appli
Sequence 9, Appli
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Sequence 444, App
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Sequence 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-905-223-89
US-08-738-367-8
US-08-737-980-1
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US-08-737-980-1
US-08-737-980-1
US-08-737-980-1
US-08-737-980-1
US-08-737-980-1
US-08-74-1
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Gapop 60.0 , Gapext 60.0
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2447
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Maximum DB s
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RESULT 3
US-09-156-425-1
; Sequence 1, Application US/09156425B
; Patent No. 5962671
; GENERAL INFORMATION:
; APPLICANT: Barker, Brenda F.
; APPLICANT: Barker, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF FAN EXPRESSION
; FILE REFERENCE: RTS-0009
; CURRENT APPLICATION NUMBER: US/09/156,425B
; CURRENT FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/737,980

FILING DATE:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

FILING DATE:

LINFORMATION FOR SEQ 1D NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 755 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3380;
                                                  Score 23; DB 1; Length 296;
Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: Fetus at 22 weeks gestation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08737980
Patent No. 5843773
GENERAL INFORMATION:
TITLE OF INVENTION: Apoptosis Regulating Gene NUMBER OF SEQUENCES: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.9%; Score 23; DB 2;
100.0%; Pred. No. 0.23;
tive 0; Mismatches (
                                        0.9%; Scor.
100.0%; Pred. No. v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                2425 ATATTTTCTCTAAAAAAAAA 2447
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                                                                                                                                                  Best Local Similarity 100.0
Matches 23; Conservative
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Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-156-425-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO ORIGINAL SOURCE:
; MOLECULE TYPE:
US-08-738-367-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3380
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US-08-737-980-1
                                                        Query Match
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                                                                                                                                                                                                                                                121 AACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT 180
                                                                                           1 TGGAGTGGGAGCTCAAGCAGGATTCTTCCCGAGTCCTGGCATCCTCAGAAGCTTCAACT 60
                                                        Gaps
                                                                                                                                  18 TGGAGTGGGAGCTCAAGCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAACT 77
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APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROFEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: BICODING THEM
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                  Length 362;
                Score 287; DB 4; Length 36;
Pred. No. 1.7e-127;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GAAAACATTGTGACCCTGGAGGACATCTATGAGAGCAC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 GAAAACATTGTGACCCTGGAGGACATCTATGAGAGCAC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATORNEY AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 base pairs
TYPE: nucleic acid
STRANDEDNESS: duble
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08738367
Patent No. 5827688
                Query Match 11.7%;
Best Local Similarity 99.7%;
Matches 337; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Massachusetts
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CLASSIFICATION: 514
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US-08-738-367-8
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100.0%; Pred. No. 2.1;
           Indels
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                                                                                                                                                                                                                 APPLICANT: Bandman, Olga
APPLICANT: Bandman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Guegler, Karl G.
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF-0321 US
                                                                                                                                                                  Sequence 12, Application US/09272796
Patent No. 6207148
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.50,
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: B111ings, Lucy J J
REGISTRATION NUMBER: 36,749
REFRENCE/POCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/08149103
; Patent No. 5750367
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                                           411 CTACACAGAGGAAGGATGCCAG 431
                                                               411 CTACACAGAGAAGGATGCCAG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1282 base pairs
         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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; CLONE: 827431
US-09-272-796-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94304
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       21;
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US-09-272-796-12
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         Matches
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                                                                                                                                                           0.9%; Score 22; DB 2; Length 755; 100.0%; Pred. No. 0.68; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.9%; Score 21; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER FRADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: B111109, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-845-4166
TELEX:
                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08878989
Patent No. 5885803
GENERAL INFORMATION:
                                                                                                                                                                                                                                2426 TATTTTCTCTAAAAAAAAA 2447
                                                                                                                                                                                                                                                      726 TATTTTCTCTAAAAAAAAA 747
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SEQUENCE CHARACTERISTICS:
LENGTH: 1282 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                       polyA_signal
713..718
                                                                                                                                                                             Best_Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TISSUE TYPE: Liver FEATURE:
                                     CDS
35..559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: PROS
CLONE: 827431
                                                  COCATION:
FEATURE:
NAME/KEY:
LOCATION:
US-08-737-980-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304
                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                     US-08-878-989-12
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Length 3116;
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US-08-456-647B-5/C

Sequence 5, Application US/08456647B

Patent No. 5811516

Patent No. 5811516

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,647B
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US/08/237,401
FILING DATE: 02-MAY-1994
PRIOR APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
PRIOR APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07251/007002
TELECOMMUNICATION INFORMATION:
             CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/451,883
FILING DATE: May 26, 1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/149,103
FILING DATE: No. 5798209ember 8, 1993
ATTORNEY/AGENT: No. 5798209ember 8, 1993
ATTORNEY/AGENT: NEVERMATION:
NAME: Knight, Matthew W.
REGISTRATION NUMBER: 35,846
REFERENCE/DOCKET NUMBER: 212/268
TELECHONE: (213) 489-1600
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20; DB 1;
Pred. No. 6.2;
OPERATING SYSTEM: IBM MS-DOS (Version 6.22) SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 GGCCCTGTGCCTGCTC 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3116 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-08-451-883-2
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US-08-451-883-2

Sequence 2, Application US/08451883

Patent No. 5798209

GENERAL INFORMATION:

APPLICANT: Lawrence C.B. Chan

TITLE OF INVENTION: HUMAN AND MOUSE VERY LOW DENSITY

TITLE OF INVENTION: LIPOPROTEIN RECEPTORS

NUMBER OF SEQUENCES: 4

CORRESPEDINCE ADDRESS:

ADDRESSEE: LYON & LYON

STREET: 633 West fifth Street, Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 2001-2066
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                    APPLICANT: Lawrence C. B. Chan
TITLE OF INVENTION: HUMAN AND MOUSE VERY LOW
TITLE OF INVENTION: HUMAN AND MOUSE VERY LOW
TITLE OF INVENTION: DENSITY LIPOPROTEIN RECEPTORS
TITLE OF INVENTION: RECEPTORS
TITLE OF INVENTION: RECEPTORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURKENT APPLICATION DATA:
CURKENT APPLICATION DATA:
FILING DATE:
CLASSIFCATION TATA:
PRIOR APPLICATION DATA:
TELING DATE:
APPLICATION NUMBER:
TELING DATE:
APPLICATION NUMBER:
TELING DATE:
TELECHANICATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 204/052
TELECHANUMICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3116 base pairs
TERNOTHER : 316 base pairs
TERNOTHER : 101clet caid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIF: 90071-2066
COMPUTER READBALE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Pred. No.
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Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
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US-08-149-103-2
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100.0%; Pred. No. 6.2;
            Indels
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                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
APPLICANT: Scadden, David T.
APPLICANT: Baker, Kevin P.
TITLE OF INVENTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Preu. ...
            Mismatches
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CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/445,640
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/17058
FILING DATE: 20-DEC-1993
PRIOR APPLICATION NUMBER: 08/157563
ATTORNEY/AGENT INFORMATION:
NAMME: HASAK, JANGT E.
REGISTRATION NUMBER: 28,616
                                                                                                                                                                                                                                                                                                                                                                     STREET: 460 Point San Bruno Blvd CITY: South San Francisco SPATE: California CONTRY: USA
                                                                                                                                                                US-08-445-640-9/c
; Sequence 9, Application US/08445640
; Patent No. 5709858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 9, Application US/08170558; Patent No. 6001621; CENERL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
            ;
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                                                 1317 TGGCTGCTCCTCCAGCTGCC 1336
                                                                       2789 TGGCTGCTCCAGCTGCC 2770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 85.
TELECOMMUNICATION INFORMATION:
TELEFHONE: 415/952-981
TELEFAX: 415/952-981
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2632 TGGCTGCTCCTCCAGCTGCC 2613
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Best Local Similarity 100.0
Matches 20; Conservative
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            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94080
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US-08-170-558-9/c
        20;
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          Matches
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Ouery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT. Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Johla
CTATE: CA
COUNTRY: US
ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUFTAMENT STATEM: TO TOST MENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,401A
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/4,486
FILING DATE: 105-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAMME: Haile Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/007001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-237-401A-5/c
Sequence 5, Application US/08237401A
Patent No. 5837448
                                                                                                                                                                                                                                                                                                                                                                             2789 IGGCIGCIGCTCCAGCIGCC 2770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEC ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3307 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; S
100.0%;
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3307 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                   CDS
237..2859
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237..2859
                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA
IMMEDIATE SOURCE:
CLONE: TYPO-3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
CLONE: Tyro-3
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                                                                                                                                                                                                                     ; LOCATION:
US-08-456-647B-5
                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-237-401A-5
                                                                                                                                                                              FEATURE
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08445461

Patent No. 6096527

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.

APPLICANT: Mark, Melania R.

APPLICANT: Baker, Kevin P.

APPLICANT: Baker, Kevin P.

TITLE OF INVENTION: Protein Tyrosine Kinases

NUMBER OF SEQUENCES: 35

CORRESPONDENCES: 35

CORRESPONDENCES: ADDRESSE:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 22-MAY-1995
ON: 530
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APPLICATION NUMBER: 08/170558
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/157563
FILING DATE: 23-NOV-1993
ATTONNEY/AGENT INFORMATION:
                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRICATION NUMBER: 08/170558
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/157563
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          FILING DAIL.
ATTORNEY/AGENT INFORMALL.
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 28,616
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,425-1896
TELEFAX: 910/371-7168
; INFORMATION FOR SED ID NO: 9:
SEQUIENCE CHARACTERISTICS:
LENGTH: 3785 bases
; LENGTH: 3785 bases
; TYPE: nucleic acid
; TAPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 85.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1317 IGGCIGCTGCTCCAGCIGCC 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2632 TGGCTGCTCCAGCTGCC 2613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22 CLASSIFICATION:
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US-08-445-461-9/c
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APPLICANT: Scadden, David T.
APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
TITLE OF INVENTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
ZIP: 94080
CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                          ZIP: 940BU
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,558
FILING DATE: 20-DEC-1993
CLASTIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 193
ATTORNEY AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 854C1
TELEPHONE: 415/25-1896
TELEX: 910/371-7168
INFORMATION FOR SED ID NO: 9:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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US-08-447-314-9/C
| Sequence 9, Application US/08447314
| Patent No. 6087144
| GENERAL INFORMATION:
| APPLICANT: Scaden, David T. APPLICANT: Barch, Will F. TITLE OF INVENTION: Protein Tyrosine Kinases | NUMBER OF SEQUENCES: 35 | CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: Genentech, Inc. STREET: 460 Point San Bruno Blvd | CITY: California | COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
APPLICATION NUMBER: US/08/447,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2632 TGGCTGCTGCTCCAGCTGCC 2613
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STRANDEDNESS: single
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US-08-170-558-9
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Job time : 120 secs
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                                                                                                                                                                                                                                                                                                                                              0.8%; Score 20; DB 3; Length 3785; 100.0%; Pred. No. 6.2; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-466-120-1

Sequence 1, Application US/08466120

Patent No. 5869284

GENERAL INFORMATION:

APPLICANT: CAO, FT AL.

TITLE OF INVENTION: Retinoic Acid Receptor Epsilon
NUMBER OF SOUGHCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STRATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COUNTRY: USA

ZIP: MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER. EADABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: WORD PERFECT 5.1

COMPUTER: WORD PERFECT 5.1

COMPUTER: JUME 6, 1995

CLASSIFICATION NUMBER: PCT/US94/07266

FILING DATE: JUN 94

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 36,134

REEFERENCE/OCCHI NUMBER: 35,134

REFERENCE/OCCHI NUMBER: 36,134

REGISTRATION NUMBER: 36,134

RESERRENCE/OCCHI NUMBER: 36,134

RESERVENCE/OCCHI NUMBER: 36,134
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3785 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-445-461-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1317 TGGCTGCTCCTCCAGCTGCC 1336
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                                                                                                                                                                                                                                                                                                                                       Query Match 0.89
Best Local Similarity 100.0
Matches 20; Conservative
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STRANDEDNESS: SINGLE
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MOLECULE TYPE: CDNA
US-08-466-120-1
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Search completed: March 15, 2003, 05:02:39

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein March 14, 2003, 14:08:41 ; Search time 16 Seconds
 (without alignments)
 1371.239 Million cell updates/sec Run on:

US-09-960-643-2 Perfect score: Title:

1 MGRKEEDDCSSWKKQTTNIR.....VKASGSSHCRAGQTGVCLIM 476 Sequence:

199416 seqs, 46092074 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 5. Appli		Sequence 2, Appli		4			16,			۱,		Sequence 2, Appli		Sequence 2. Appli	Segmence 2. Appli	Sequence 6. Appli	٠,	٠, ه
	ID	US-09-935-464-5	US-09-935-464-3	US-10-024-036B-2	US-10-142-356-7	US-09-817-181-4	US-09-935-464-36	US-09-817-181-2	US-09-835-788A-16	US-09-797-039-2	US-10-153-921-2	US-10-217-357-4	US-09-975-326-4	US-09-934-406-2	US-10-217-357-2	US-09-975-326-2	US-10-116-332-2	US-10-142-356-6	US-10-096-960-4	US-10-024-036B-5
	DB	. 6	0	σ	0	10	6	10	10	10	12	6	10	σ	σ	10	δ	σ	12	6
	Query Match Length DB	476	460	357	370	370	317	326	280	501	501	765	765	992	992	166	385	545	556	648
	Query	100.0	4.0	9.6	5.9	5.9	5.8	7.0	9.7	7.6	7.6	24.9	4.9	4.9	4.9	4.9	4.1	3.7	3.6	3.3
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	Score	2513	2362	1246	1152.5	1152.5	1151	1016.5	944.5	747.5	747.5	625.5	625.5	625.5	625.5	625.5	606.5	594.5	592	585.5
	Result No.	1	7	m	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19

Sequence 4, Appli Sequence 1, Appli	Sequence 2, Appli Sequence 23, Appl	Sequence 16, Appl	Sequence 11, Appl Sequence 25, Appl	Sequence 17, Appl	Sequence 5, Appli	Sequence 2, Appli	Sequence 238, App	Sequence 17, Appl	Sequence 265, App	Sequence 266, App	⋖		Sequence 39, Appl	ò	Sequence 18, Appl	Sequence 34, Appl	Sequence 18, Appl		Sequence 22, Appl	Sequence 19, Appl	188	Sequence 9, Appli
0 US-09-740-627-1	.2 US-10-096-960-2 US-09-988-462-23	US-10-081-119-16		10 US-09-854-731-17	.0 US-09-922-138-5	.0 US-09-841-683-2	.0 US-09-771-161A-238	.0 US-09-858-664A-17	.0 US-09-771-161A-265	.0 US-09-771-161A-266	_			10 US-09-771-161A-210		_		.0 US-09-854-731-4	_	10 US-09-854-731-19	.0 US-09-771-161A-188	0 US-09-740-627-9
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20 5	23 2		26 5		28	29	30	31	32	33	34 5	35 5	36	37 5	38 5	39	40 4	41 4	42	43	44	45 4

ALIGNMENTS

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APPLICANT: Meyer, Joanne
APPLICANT: Barrington Martin, Rory
APPLICANT: Barrington Martin, Rory
APPLICANT: Parker, Alexander
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYC
TITLE OF INVENTION: DISCORDERS SUCH AS SCHIZOPHRENIA
TITLE OF INVENTION: DISCORDERS SUCH AS SCHIZOPHRENIA
CURRENT APPLICATION NUMBER: US 09/0935,464
CURRENT FILING DATE: 2001-08-23
FRIOR PLILNG DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 476
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100.0%; Pred. No. 1.3e-181;
Live 0; Mismatches 0;
                 ; Sequence 5, Application US/09935464; Publication No. US20030027153A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               Matches 476; Conservative
                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-09-935-464-5
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
US-09-935-464-5
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61 GKESSIENEIAVLRKIKHENIVALEDIYESPNHLYLVMQLVSGGELFDRIVEKGFYTEKD 120
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; Pred. No. 2.6e-86;
40; Mismatches 45; Indels
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Sequence 7, Application US/10142356
Publication No. US20030036183A1
GENERAL INFORMATION:
APPLICANT: Boylan, John F.
APPLICANT: Bowers, Alex J.
TITLE OF INVENTION: Serine-Threonine Kinase Member, h2520-40
FILE REFERENCE: 01017/3717A
CURRENT APPLICATION NUMBER: 2002-05-09
PRIOR APPLICATION NUMBER: 60/290,276
PRIOR FILING DATE: 2001-05-10
NUMBER: OF THE CONTROL OF THE CONTROL
                                                                                                                                                                     Sequence 2, Application US/10024036B
Fublication No. US20030028004A1
GENERAL INFORMATION:
TITLE OF INVENTION: Rajasekhar
TITLE OF INVENTION: RAJASSAN and 69112, Protein Kinase
TITLE OF INVENTION: MOLECULES and USES THEREFORE
TITLE OF INVENTION: MOLECULES and USES THEREFORE
CURRENT APPLICATION NUMBER: US/10/024,036B
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/25822
FRIOR APPLICATION NUMBER: 60/25822
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTERO for Windows Version 4.0
                           SCENIGSKGKSSYCSEPTLLKKANKKQ 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAKSKWRQAFNAAAVVHHMRKLHM 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 73.1%;
Matches 237; Conservative 40
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-024-036B-2
                                                                                                                               RESULT 3
US-10-024-036B-2
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LENGTH: 357
TYPE: PRT
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US-09-935-464-3
US-09-935-464-3
Sequence 3, Application US/09935464
Publication No. US20030027153A1
GENERAL INFORMATION:
APPLICANT: Meyer, Joanne
APPLICANT: Meyer, Joanne
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/14702 US.
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT PILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR APPLICATION TO BATE: US 09/757,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                     LDHSVALPALTQLPCQHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCCS 420
                                                                                                                                                                                                                                                              PFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFA 300
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100.0%; Pred. No. 3e-170;
Live 0; Mismatches 0;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
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Best Local Similarity 100.
Matches 447; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Meyer, Joanne
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYR
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/JH70Z US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT APPLICATION NUMBER: US 09/757,300
PRIOR PILING DATE: 2001-08-23
PRIOR PILING DATE: 2001-09-30
SECIENCE: PALENTING DATE: 2001-01-09
NUMBER: OF SECIENCE: 3300
SOFTWARE: PALENTING VERSION 3.0
SECIENCE OF SEC
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; Pred. No. 3.2e-79;
44; Mismatches 51;
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Best Local Similarity 69.4'
Matches 220; Conservative
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ORGANISM: Homo sapiens
US-09-935-464-36
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Patent No. US20020142427A1
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001189
CURRENT APPLICATION NUMBER: US/09/817,181
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASESEQ for Windows Version 4.0
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55.8%; Pred. No. 3e-79;
wismatches 62; Indels
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                                                                         45.9%; Score 1152.5; Di 55.8%; Pred. No. 3e-79;
                                                                                                                         46; Mismatches
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                                                                                             Best_Local Similarity
Matches 239; Conserv
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ORGANISM: Human
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; ORGANISM: H
US-10-142-356-7
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Length 317;

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70 AVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLS 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAK 301
                                                                                                                                                                                                                                                                                                                                                           97 MQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEE 156
                                                                                                                                                                                                                                                                                                                                       157 NSKIMITDFGLSKMEQNG-IMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCG 215
                                                                                                                                                                                                                                                                                                                                                                                                                         YPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHP 275
                                                                                                                                                                                                                                                                           15 QTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRD----SSLENEI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 OPSEVTDRYDLGOVIKTEEFCEIFRAKDKTTGKLHTCKKFOK----RDGRKVRKAAKNEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 VLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETE-----SKLFEKIKEGYYEFESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09797039

Sequence 2, Application US/09797039

Patent No. US2002004209941

GENERAL INFORMATION:

APPLICANT: Clandt, Peter J.

APPLICANT: Rapeller Libermann, Rosana
TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR

FILE REPERBENCE: 1044e-017001

CURRENT APPLICATION NUMBER: US/09/797,039

CURRENT FILING DATE: 2001-02-28

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEO for win Anner.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                  DB 10;
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                                                                                                                                                                  Query Match 37.6%; Score 944.5; DB 1
Best Local Similarity 77.5%; Pred. No. 9.7e-64;
Matches 176; Conservative 26; Mismatches 24
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               SOFTWARE: PatentIn Ver. 2.0
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NUMBER OF SEQ ID NOS:
                                                                                                    ORGANISM: HOMO
                                                                                                                          US-09-835-788A-16
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LENGTH: 501
TYPE: PRT
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                                        SEQ ID NO 16
LENGTH: 280
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US-09-797-039-2
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Best Local 8
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ITILE OF INVENTION:
APPLICANT: Ni et al.

ITILE OF INVENTION: Death Domain-Containing Receptor Polynucleotides, Polypeptides, TITLE OF INVENTION: Antibodies
FILE REFERENCE: PT018P1
CURRENT APPLICATION NUMBER: US/09/835,788A
CURRENT FILING DATE: 2001-04-17
PRIOR PILING DATE: 2000-10-17,7US00/28666
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-11-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 FRD------VLGTIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERD 73
                                                                                             Sequence 2, Application US/09817181
Patent No. US20020142427A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, TITLE OF INVENTION: THEREOF
FILE OF INVENTION: THEREOF
FILE REFERENCE: CL001189
CURRENT FILION DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2.5
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Best Local Similarity 55.7%; Pred. No. 4.5e-69;
Matches 211; Conservative 34; Mismatches 47; Indels
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Patent No. US20020077458A1
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301 AVVRHMRKLQLGTSQEG
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 326
TYPE: PRT
ORGANISM: Human
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Sequence 4, Application US/09975326; Patent No. US20020128458A1; GENERAL INFORMATION:
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                                                                                                                     DSTAPEGATG 477
                                                                                        462 SSHCRAGQTG 471
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US-10-217-357-4
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 4
LENGIH: 765
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Patent No. US20020142430A1

GENERAL INFORMATION:

TOTAL OF INVENTION: Chubhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLO00612DIV

CURRENT FILING DATE: 2002-05-24

PRIOR PILING DATE: 2000-05-30

PRIOR PLICATION NUMBER: 09/734,030

PRIOR PLICATION NUMBER: 09/734,030

PRIOR PLICATION NUMBER: 09/734,030

PRIOR PLICATION NUMBER: 300-012-12

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2
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                                                                                                                                                                      130 AVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPE 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKWKKAVRVTTLMKRLR------APEQSSTAAAQSASATDTATPGAAGGATAAAA 359
251 YWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFAR 310
                                                           -----RAPE--QSSTAAAQSASATDTATPGA 350
                                                                                                                      351 AGGATAAAASGATSAPEGDAARAAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSI 410
                                                                                                                                                   412 AAGPCGCCSSCLN----IGSKGKSSYCSEPTLLKKANKKQNFKSEVMV---PVKASGSSH 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 AVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLS 129
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                              SKWRQAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVL
                                                                                         --- DHSVALPALTQLPCQHGRRP----TAPGGRSLNCLVNGSL--HISSSLVPMHQGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.7%; Score 747.5; DB 12; Length 35.3%; Pred. No. 1.5e-48; Live 86; Mismatches 170; Indels
                                                           311 AKWKKAVRVTTL---MKRL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 35.3%
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-10-153-921-2
                                                                                                                                                                                                                CRAGQTG 471
                                                                                                                                                                                                                                             471 APEGATG 477
                                                                                                                                                                                                                                                                                           RESULT 10
US-10-153-921-2
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Sequence 4, Application US/10217357

Sequence 4, Application US/10217357

Publication No. US20030023063A1

GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
TITLE OF INVENTION: Same
TITLE OF INVENTION: Same
CURRENT APPLICATION NUMBER: US/10/217,357

CURRENT APPLICATION NUMBER: US/208-09

PRIOR FILING DATE: 2001-10-11

PRIOR PELING DATE: 2000-10-12

PRIOR APPLICATION NUMBER: US 60/239,821

PRIOR APPLICATION NUMBER: US 60/239,821

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASESEQ for Windows Version 4.0
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                                                         L-----AAGPCGCCSSCLNIGSKGKSSYCSEPTLLKKANKKQNFKSEVMV---PVKASG 461
                                                                                                               ---ATDGRATPATEESTVPTTQSSAMLATKAAATPEPAMAQP 467
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2 GRKEEDDCSSWK----
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US-10-217-357-2
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US-10-217-357-2
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         APPLICANT: Mathur, Brian
TITLE OF INVENTION: No. US20020128458Alel Human Kinases and Polynucleotides Encoding
FILE REFERENCE: LEX-0254-038
CURRENT APPLICATION NUMBER: US/09/975,326
CURRENT FILING DATE: 2001-10-11
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 765
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Fublication No. US20020192204A1
GERREAL INFORMATION:
TITLE OF INVENTION: 15985, A NOVEL HUMAN SERINE/THREONINE
TITLE OF INVENTION: PROTEIN KINASE FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-078001
CURRENT APPLICATION UNBABE: US/09/934,406
CURRENT FILING DATE: 2001-08-21
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ for Windows Version 4.0
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24.9%; Score 625.5; DB 10;
Best Local Similarity 34.8%; Pred. No. 4.1e-39;
Matches 142; Conservative 82; Mismatches 143;
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APPLICANT: Turner, C. Alexander Jr.
                                                                                                                                                                                   TYPE: PRT
ORGANISM: homo sapiens
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LENGTH: 766
TYPE: PRT
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Squence 2, Application US/10217357
Squence 2, Application No US2003002306341
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Wathur, Brian
TITLE OF INVENTION: No. US20030023063Alel Human Kinases and Polynucleotides Encodi
TITLE OF INVENTION: Same
FILE REFERENCE: LEX-0254-USA
CURRENT APPLICATION NUMBER: US/09/975,326
FRICK APPLICATION NUMBER: US 60/239,821
PRIOR PLING DATE: 2001-10-11
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 4
SOCTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 766 11; |: ::|||::|| | DKAKCCGKEHLIENEVSILRRVKHPNIIMLVEEMETATELFLVWELVKGGDLFDAITSST 485 114 VYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLT-PEENSKIMITDFGLSKMEQ 172 55 KKSPAF-RDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERG 113 604 VSLQIQKNF--AKSKWRQAFNAAAVVHHMR-----KLHMNLH-----SPGVRPEVENRPP 338 366 GGPELDRCISPEGVNGNRCSESSTLLEKYKIGKVIGDGNFAVVKECIDRSTGKEFALKII 425 55 KKSPAF-RDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERG 113 VYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLT-PEENSKIMITDFGLSKMEQ 172 54 Gaps 2 GRKEEDDCSSWK-----KQTTNIRKTFIFWEVLGSGAFSEVFLVKQRLTGKLFALKCI 54 173 NGIMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEET--ESKLFEK ---KQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI 41; Length 766; 339 ETQASETSRPSSPEITITEAPVLDHSVALPALTQLPCQHGRRPTAPGG 386 -----SVEEIPVPGEAVPAPTPPESPTPH-CPPAAPGG 755 Indels Query Match 24.9%; Score 625.5; DB 9; Best Local Similarity 34.8%; Pred. No. 4.1e-39; Matches 142; Conservative 82; Mismatches 143; q

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RESULT 15
US-09-975-326-2
US-09-975-326-5
Patent No. US20020128458A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
TITE OF INVEWTION: No. US20020128458A1el Human Kinases and Polynucleotides Encoding
TITE OF INVEWTION: No. US20020128458A1el Human Kinases and Polynucleotides Encoding
TITE OF INVEWTION: No. US20020128458A1el Human Kinases and Polynucleotides Encoding
CURRENT APPLICATION NUMBER: US/09/975,326
CURRENT FILING DATE: 2001-10-11
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 766
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                                                                                                             173 NGIMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEET--ESKLFEK 230
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55 KKSPAF-RDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERG 113
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                                                                                   291 VSLQIQKNF--AKSKWRQAFNAAAVVHHMR-----KLHMNLH-----SPGVRPEVENRPP 338
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                                                                                                                                                                                          Search completed: March 14, 2003, 14:10:54
Job time : 19 secs
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CORGANISM: homo sapiens
US-09-975-326-2
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/product= "Human CAMK-X1 protein"
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                                                 AAD36148
AAD36155
AAD36157
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ABC24014
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ABC24015
AAF74277
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AAH13806
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70..1500
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2000US-237419P.
2000US-237423P.
2000US-238558P.
2001US-290555P.
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  44888444444400107044000440400044410000
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02-OCT-2000; 2
02-OCT-2000; 2
04-OCT-2000; 2
10-MAY-2001; 2
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(without alignments)
9736.113 Million cell updates/sec
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1. (SIDS2)gcgdata/geneseq_geneseqn_embl_/NA1980.DAT:*

2. (SIDS2)gcgdata/geneseq_geneseqn_embl_/NA1981.DAT:*

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16. (SIDS2)gcgdata/geneseq_geneseqn_embl_/NA1981.DAT:*

17. (SIDS2)gcgdata/geneseq_geneseqn_embl_/NA1991.DAT:*

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29. (SIDS2)gcgdata/geneseq_geneseqn_embl_/NA1991.DAT:*

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The invention relates to a method for screening biologically active agent that modulates cancer associated protein kinase function. The invention also relates to a method for diagnosing cancer comprising determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase. The method is useful for diagnosing cancer. A protein kinase is useful for screening biological agents that modulate cancer associated protein kinase function. Downregulating the activity of protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon cancer. A nucleic acid encoding protein kinase is useful to screen biopsy derived tumours and inflammatory samples such as atthritic synovium, for amplified DNA in the cell or increased expression of corresponding mRNA or protein and is also useful to detect differences in expression levels such as molecular weight, amino acid and nucleotide sequences between the vocalis. The present sequence is human calmodulin kinase CAMK-XI gene located on chromosome 1737, 1-37, 2 Diagnosing cancer, comprises determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase or upregulation of expression of the protein kinase, in the cancer Claim 16; Page 62-64; 87pp; English. located on chromosome 1q32.1-32.3. KINETEK PHARM INC. UNIV BRITISH COLUMBIA. Delaney AD; 2002-394145/42. P-PSDB; AAE22764. Yoganathan T, (KINE-) ((UYBR-) (

Sequence 2447 BP; 590 A; 707 C; 604 G; 546 T; 0 other;

ö 540 CTGGAGGCAATGGGTCGAAAGGAAGATGACTGCAGTTCCTGGAAGAAACAGACCACC 120 180 240 CAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAG 420 420 Gaps 9 9 TGGAGTGGGAGCTCAAGCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAACT **AACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT** TTCCTGGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCA CCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAAAGATCAAGCAT **AAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAGAAT** GGCATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTTACCCTGAAGAAC ö 24; Length Indels ; 0 DB 100.0%; Score 2447; 100.0%; Pred. No. 0; 0; Mismatches Matches 2447; Conservative Best Local Similarity Query Match н 61 121 61 181 181 241 301 361 361 121 301 421 481 481 421 OD ò В οy g oy Dp δ a ò g õ g ò g ò

CTTCCAAACCTGGTGTCTATCCGGCAGAGGGAAGGCAGAGCAAGTGGAGCAGGGCTT 1620 AGCAGGAGCAGTTTCTGGCCAGAAGCACCAGCCTGCTGCCAGCGGGGCAGCCCCTCATAG 1680 780 CCTGAAACTCAAGCCTCAGAAACCTCTAGACCCCAGCTCCCCTGAGATCACCATCACCGAG CTTGAGAAGGATCCGAACGAGCGGTACACCTGTGAGAAGGCCTTGAGTCATCCCTGGATT AACTTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGCACCACATG CCTGAAACTCAAGCCTCAGAAACCTCTAGACCCAGCTCCCCTGAGATCACCATCACCGAG ACTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAGC CCGTTCTATGAAGAAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGGGCTACTATGAG TITGAGTCTCCATTCTGGGATGACATTTCTGAGTCAGCCAAGGACTTTATTTGCCACTTG AGGAAGCTACACATGAACCTGCACAGCCCGGGCGTCCGCCCAGAGGTGGAGAACAGGCCG GGCCGCCGCCCACTGCCCCTGGTGGCAGGTCCCTCAACTGCCTGGTCAATGGCTCCCTC ACACTCCTCAAAAAGGCCAACAAAAAACAGAACTTCAAGTCGGAGGTCATGGTACCAGTT TTCCTGGAGCCTGTGCCTATGTCACTGCAATTTTCAGGAGACATATTCAACTCCTCTGCT CTTCCAAACCTGGTGTCTATCCGGCAGAGGAGGAGGAAGCAGAGCAAGTGGAGCACGGCTT AAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCCC TGCTGCTCCAGCTGCCTGAACATTGGGAGCAAAGGAAAGTCCTCCTACTGCTCTGAGCCC 1081 1261 901 1021 1021 1141 1201 1321 1381 601 601 661 661 721 781 781 841 961 961 1081 1141 1261 1321 1381 1441 1441 1501 1501 721 901 1201 1561 1561 1621 a ŏ g ŏ a οχ Ob δ Q δ ρp ò Ω δ Q ŏ qq δ οq φ g ŏ g οy g Óγ g Qγ qq δ qq ά qq ŏ qq ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; hautington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                     CGGTGGCTCTGTGCAGTGTACGTAGATAGCTCTCGCCTGGGTCTGTGCTGTGTTTGTCGTGA
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                               GAGGCCCAGGAGGCACCCCAAGGCGTAGAAGCCTTGTTGAAGCTGTGAGCAGGAGAAGC
                                         GGTGCCCACCAGCTTCCAGGTCTCCCTGACCTGCCTGCTCTATGCCCCACACACCCTACGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                 polypeptides, useful for treating disorders system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 GGACAGCAGCCTGGAGAATGAGATTGCTGTGTAAAAAAGATCAAGCATGAAAAACATTGT
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Zhang J
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Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 4692; 10078pp; English.
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Wehrman T, Xu
Goodrich R,
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GGACATCTATGAGAG 	AGCTCTTTGACCGGAT	CCAGCAGGTCTTGTC 	TAAAGCCCGAAAACCT 	CTTTGGTCTGTCC 	CTACGTGGCTCCAG 	CATCGGCGTCATCA 	GAGTCTAAGCTTTTCGA 	AGT	CGAGCGGTACACCTGTGA 	CCGGGACATCTACO 	GAGGCAAGCCTTCAACC 	GCACAGCCCGGGCGT 	AAACCTCTAGACCCAGG	GTGTAGCACTCCCTGC 	TGGTGGCAGGTCCCT(GCCCATGCATCAGG 	CATTGGGAGCAAAG
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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        AAAGGCCAACAAAAAAACAGAACTTCAAGTCGGAGGTCATGGTACCAGTTAAAGCCAGTGG
                                          CAGCTCCCACTGCCGGGCAGGGCAGACTGGAGTCTGTCTTTATGTGATTCCTGGAGCC
                                                                    TGTGCCTATGTCACTGCAATTTTCAGGAGACATATTCAACTCCTCTGCTCTTCCAAACCT
                                                                             GGTGTCTATCCGGCAGAGGGAGGCAGGCAGGCAAGTGGAGCAGGGCTTAGCAGGAGCAG
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Zhang J;
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Yang Y,
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Xu C, Xue AJ,
, Drmanac RT;
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Wehrman T, Xu
Goodrich R,
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2000US-055317.
2000US-0598042.
2000US-0653150.
2000US-0653450.
2000US-0662191.
2000US-0653036.
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P-PSDB; AAM39761.
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Wang Z, F
Zhou P,
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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Wang J, W
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                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system disease, such as lateal sclerosis, and Shy-Draqer Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotexic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed
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46.8%; Score 1144; DB
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1294; Conservative 0; Mismatches
                                        SEQ ID NO 1120; 10078pp; English.
    system injuries
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leukaemia;
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                  1428 TGGCAGGTCCCTCAACTGCCTGGTCAATGGCTCCCTCCACATCAGCAGCAGCTGGTGGCC
                                                                                          CATGCATCAGGGGTCCCTGGCCGCCGGGCCCTGTGCTGCTGCTCCAGCTGCCTGAACAT
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1224 TGGCAGGTCCCTCAACTGCCTGGTCAATGGCTCCCTCCACATCAGCAGCAGCCTGGTGCC
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2000US-0184697.
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Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC; Chen A, D'Sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE; Bufour GE, Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones AL; Liu TF, Roseberry AM, Rosen BH, Russo FD, Stockdreher TK, Daffo A; Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W; Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;
                          2000US - 0184776.
2000US - 018481777.
2000US - 01848137.
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2000US - 0185216.
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Liu TE, Rose
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The invention relates to polynuclectides (I) encoding diagnostic and therapeutic (DTTHP) polypeptides (II), which include e.g. enzymes, and proteins involved in growth and development and treatment of diseases (II) may be used in the prevention, diagnosis and treatment of diseases (II) may be used to treat disorders associated with decreased polypeptide expression by rectifying mutations or deletions in a patient's genome, that affect the activity of the DITHPS, by expressing inactive proteins or supplementing the patient's own production of them. (I) and (II) may be used to treat diseases, for example, cell proliferative disorder, crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma, leukaemia, autoimmune disorders, and respiratory disorders. Additionally, (I) may be used to produce the DITHPS, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of them captured against DITHPs and in assays to identify modulators of DITHP expression and activity. The anti-DITHP antibodies and antagonists may also be used as diagnostic agents for detecting the presence of DITHPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAS30986-AAS31196 represent human diagnostic and therapeutic (DITHP) polynucleotides of the invention. Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics Claim 1; Page 310-311; 522pp; English.

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31.5%; Score 772; DB 22; Length 2689;
Sequence 2689 BP; 642 A; 748 C; 678 G; 621 T; 0 other;
                                                           Query Match
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       Gaps
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                                                                                                     GGCATCCTCAGAAGCTTCAACTCTGGAGGCAATGGGTCGAAAGGAAGAAGAAGATGACTGCAG
                                  TGTGTTGAAAAAGATCAAGCATGAAACATTGTGACCCTGGAGGACATCTATGAGAGCAC
                                                                                                                                                                           GCTGGCCCAGAAACCCTACAGCAAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTA
                                                                                              TCTGAAGTGCATCAAGAAGTCACCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGATTGC
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        Indels
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        Mismatches
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99.98;
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        Conservative
Similarity
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05-DEC-2000;
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05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
       nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                    20000US - 0.179065.
20000US - 0.18664.
2000US - 0.18664.
2000US - 0.18664.
2000US - 0.198174.
2000US - 0.216846.
2000US - 0.216847.
2000US - 0.225266.
2000US - 0.225266.
2000US - 0.225266.
2000US - 0.225266.
2000US - 0.225267.
2000US - 0.225266.
2000US - 0.225266.
2000US - 0.225266.
2000US - 0.225268.
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2000US - 0.225758.
2000US - 0.225768.
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2000US-0232399.
2000US-0232400.
2000US-0232401.
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                                                                                                                                                                                                                                                                  31 - JAN - 2000; 24 - FEB - 2000; 25 - MAR - 2000; 26 - MAR - 2000; 27 - MAR - 2000; 28 - JUL - 2000; 28 - JUL - 2000; 26 - JUL - 2000; 27 - MG 
                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                      17-JAN-2001;
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20000S-0246525 20000S-0246525 20000S-0246525 20000S-0246528 20000S-0246528 20000S-0246632 20000S-0246610 20000S-0246611 20000S-0246611 20000S-0246611 20000S-0246612 20000S-0249209 20000S-0249209

2000US-0246478. 2000US-0246523. 2000US-0249211. 2000US-0249212. 2000US-0249213.

2000US-0249214. 2000US-0249215. 2000US-0249216. 2000US-0249216.

2000US-0249218. 2000US-0249244. 2000US-0249245.

20000S-0249264. 20000S-0249265. 20000S-0249297. 20000S-0249299. 20000S-0249300.

2000US-0250160. 2000US-0250391. 2000US-0251030. 2000US-0251988. 2000US-0256719.

2000US-0251479 2000US-0251856

2000US-0233063.
2000US-0233064.
2000US-0234023.
2000US-0234624.
2000US-0234694.
2000US-0234997.
2000US-0234997.
2000US-0235834.
2000US-0235834.
2000US-0235834.
2000US-02363636.
2000US-0236369.
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2000US-0236369.
2000US-0236369.
2000US-0236369.
2000US-0236369.
2000US-0234041787.
2000US-02411865.

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Dy (1), are used to treat a medition to disposed or treated include authological condition. Disorders which are disposed or treated include authological condition. Disorders which are disposed or treated include disorders e.g. neoplasms of the breast or liver, cardiovascular disorders c.g. cardiac arrest, carebrovascular disorders e.g. disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired inmenodeficiency virus (AIDS) and fundi, ocular disorders e.g. dasheds e.g. denocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituliary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders e.g. nonallergic rhinitis, renal disorders e.g. respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. nonallergic chinitis, renal disorders e.g. festinate and blood related disorders e.g. myocardial fraction. The polypeptides can also be used to aid wound healing and cantiation organs before transplantation, for supporting cell culture of primary tissues, to respense a feroporting cell culture of primary tissues, to respense as food additive or preservative to
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                                                                                                                                                                                                                                                                                                                                                                                        invention describes an isolated nucleic acid molecule (I) encoding a el central nervous system protein. (I) and polypeptides (III) encoded (I), are used to treat a medical conditions and in diagnosis of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                increase or decrease storage capabilities, fat content, lipid, protein,
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                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives
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                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 70; 837pp; English.
                                                                                                                                                                           Ruben SM;
                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                    2000US-0251990.
2000US-0254097.
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                                                                                                2001US-0259678
                                   2000US-0251989
              2000US-0251869
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Matches 355; Conservative
                                                                                                                                                                         Rosen CA, Barash SC,
                                                                                                                                                                                                               WPI; 2001-581633/65.
P-PSDB; AAU87150.
                                                      08-DEC-2000;
11-DEC-2000;
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              08-DEC-2000;
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human secreted proteins, and encode the proteins given in AAY13297 to AAY13219, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid are an also be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proliferation/differentiation activity, hamatopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, tomore growth regulating activity, mammatory activity, tumour inhibition activity or other activities activity, conceptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping promoter or sequences can also be used for obtaining corresponding promoter in directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
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                                                                                                                                                                                          forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAACAGACCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated brain-derived nucleic acids - used to develop products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TGGAGTGGGAGCTCAAGCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAAACT
                                                                                                                                                                           tag; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which may have cytokine, immune, regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity
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                                                                                                                                                                             Human; secreted protein; EST; expressed sequence
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                                                                                                                                   Human secreted protein 5' EST SEQ ID NO: 52.
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                   AAX51838 standard; DNA; 362 BP
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                                                                                                 (first entry)
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                                                           AAX51838;
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AAX51838
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121 AACATCCGGAAAACCTTCATTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT 180

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20000S-0237040.
2000US-0239935.
2000US-0239937.
2000US-0240960.
2000US-0241221.
  2000US-0225758.
2000US-0225759.
2000US-0226279.
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                                                                                    cDNA encoding novel signal transduction pathway protein, Seq ID 189
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The invention relates to novel isolated polypeptides (I), and the invention relates to novel isolated polypeptides (I), and dependent of disponses including immune system changoashing preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune transplant rejections and graft versus host disease, infectious diseases (e.g. transplant rejections and graft versus host disease, infectious diseases (e.g. transplant rejections and graft versus host disease, infectious diseases (e.g. transplant rejections and graft versus host disease, infectious diseases (e.g. transplant rejections disorders (e.g. disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. dlancher's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. globomerulomephritis), cardiovascular disorders (e.g. disorders (e.g. globomerulomephritis), cardiovascular disorders (e.g. disorders (inflammatory disorders), liver disorders (erg. disorders) (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of the choner former proliferation in pathologies = g.g. acquired immune deficiency syndrome (AlbS). AAS26976-AAS2780 represent novel signal transduction cycle pathway protein coding sequences and PCR primers of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders
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                                                                                                                61 CTGGAGGCAATGGGTCGAAAGGAAGATGACTGCAGTTCCTGGAAGAAACAGACCACC 120
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                                                                                                                               AACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT
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11.2%; Score 274; DB 22; Length 476; 100.0%; Pred. No. 6.9e-123; ive 0; Mismatches 0; Indels
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Rosen CA, Barash SC, Ruben SM;
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2000US-0249245.
2000US-0249264.
2000US-0249265.
2000US-0249265.
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2000US-0250160.
2000US-0250391.
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2000US-0251856.
2000US-0251868.
2000US-0251869.
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2000US-0249217.
2000US-0249218.
                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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P-PSDB; AAU87467.
08 - NOV - 2000;

17 - NOV - 2000;
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01-DEC-2000)
05-DEC-2000)
05-DEC-2000)
05-DEC-2000)
06-DEC-2000)
06-DEC-2000)
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08-DEC-2000;
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New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 1; SEQ ID No 387; 837pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. Alzheimer's disease and ampiogenesis, nervous system disorders e.g. Alzheimer's disease and ampiotrophic lateral sclerosis, infections caused by bacteria, viruses c.g. Acquired inmennodeficiency virus (AIDS) and fungi, collar disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies,

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respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotraxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
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                                                                                                                                                                                                                                                                                                                                  180
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                                                                                                                                                                                                                                                                                                                                                                                              TICCTGGTGAAGCAAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                                                                                                                                                                                           264
                                                                                                                                                                                                                                                                                                                                                                                                               secreted protein; gene therapy; vaccine; treatment; diagnosis;
                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                       CTGGAGGCAATGGGTCGAAAGGAAGATGACTGCAGTTCCTGGAAGAAACAGACCACC
                                                                                                                                                                                                                                                                                                                                                    1 TGGAGTGGGAGCTCAAGCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAACT
                                                                                                                                                                                                                                                                        CTGGAGGCAATGGGTCGAAAGGAAGATGACTGCAGTTCCTGGAAGAAACAGACCACC
                                                                                                                                                                                                                                                                                                                                    AACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT
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                                                                                                                                               Length 476;
                                                                                                                                                                            Indels
                                                                                                                                             11.2%; Score 274; DB 23; L ilarity 100.0%; Pred. No. 6.9e-123; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jobert S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 CCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein cDNA, SEQ ID NO: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGA 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 741-742; 921pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH64901 standard; cDNA; 1361 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-DEC-2000; 2000WO-IB01938
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06-MAR-2000; 2000US-0187470
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P-PSDB; AAG89298.
                                                                                                                                                              Similarity
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                                                                                                                                                              Local Simi
hes 274;
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GENSET; ss
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                                                                                                                                                 Query Match
                                                                                                                                                                            Matches
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they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression. The sense and antisense nucleic acids may also be their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy.

The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antigonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET nucleic acid of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2359 TTCCCCAGTTTCCTCGCCCTCCACCCTCCAGCTTCATGCTCAGTGTTGTGCTTAATAAA 2418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1237 TICCCCAGTTTCCTCGCCCTCCACCCCTCCAGCTTCATGCTCATGTTGTGCTTAATAAA 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2299 TICTAATCCTGCCTCTTTCTCTCTTGAAAGTCCAGCACACCATTCTTGTCC 2358
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                                                                                                                                                                                                                                                                                                                                                  Sequence 1361 BP; 438 A; 245 C; 302 G; 375 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                        6.1%; Score 149; DB 22;
100.0%; Pred. No. 5.3e-62;
iive 0; Mismatches 0;
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2000US-229751P.
2000US-230016P.
2000US-230583P.
2000US-230505P.
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2000US-229748P.
2000US-229749P.
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Matches 149; Conservative
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05-SEP-2000;
05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
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05-SEP-2000;
05-SEP-2000;
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ABL99884
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BP.

ABN35390 standard; DNA; 60

RESULT 11 ABN35390 ABN35390;

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The invention comprises the amino acid and coding sequences of human secretory (SPTM) proteins. The SPTM DNA and amino acid sequences are useful for treating a disease or condition associated with the expression of functional SPTM. The SPTM DNA sequences are useful for somatic or germline gene therapy to correct a genetic deficiency (e.g. severe combined immunodeficiancy). The SPTM DNA sequences are also useful in providing protection against intracellular parasites (e.g. fungal are also useful for diagnosing cell proliferative disorders, cancer, ammune disorders (e.g. ALDS), neurological disorders (e.g. Parkinson's disease), motor neuron disorders, demyelinating diseases (e.g. multiple sclerosis), meningitis, abscesses, prion diseases, cerebral palsy, cenuroskeletal disorders, periphenal nervous system disorders, dermatomyositis and polymyositis, myopathy, myasthenia gravis, and mental disorders (e.g. Tourette's syndrome), cDNA sequences ABL99746 - ABL99929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Altus CM, Dufour GE, Chalup MS, Hillman JL. iht RJ, Gietzen D, Liu TF, Yap PE, Dahl CR; L. Rohatgi SD, Harris B, Roseberry AM; David MH, Panzer SR, Flores V, Daffo A; hang SC, Au AP, Inman RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide sequences encoding human secretory proteins useful for gene therapy of e.g. genetic deficiency disorders, cancers, and diseases caused by intracellular parasites -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders (e.g. Tourette's syndrome). cDNA sequences ABL99/represent human secretory polynucleotides of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 ATCAGGAGCTTTCTCAGAAGTTTTCCTGGTGAAGCAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.4%; Score 107; DB 24;
99.4%; Pred. No. 1.5e-41;
ive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Stuart J, Lincoln SE, Altus CM, CALLOS Stuart J, Lincoln SE, Altus CM, Cietzen D, Jones AL, Yu JY, Wright RJ, Gietzen D, Momiyama MG, Bradley DL, Rohatgi SD, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 331; 585pp; English.
06-SEP-2000; 2000US-230514P.
06-SEP-2000; 2000US-230515P.
06-SEP-2000; 2000US-230511P.
06-SEP-2000; 2000US-230511P.
06-SEP-2000; 2000US-230519P.
06-SEP-2000; 2000US-23059FP.
06-SEP-2000; 2000US-23059FP.
06-SEP-2000; 2000US-23059P.
06-SEP-2000; 2000US-23059P.
06-SEP-2000; 2000US-230864P.
06-SEP-2000; 2000US-23088PP.
06-SEP-2000; 2000US-23088PP.
06-SEP-2000; 2000US-23088PP.
06-SEP-2000; 2000US-23089P.
07-SEP-2000; 2000US-23099P.
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Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                  07-SEP-2000; 2000US-230951P.
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P-PSDB; ABB97887.
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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or detecting RNA transcripts and splice variants of detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised minical interaction of detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABNA7253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1526 TGCAATTTTCAGGAGACATATTCAACTCCTCTGCTCTTCCAAACCTGGTGTCTATCCGGC 1585
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                                                                                                                                                  RNA transcript;
                                                                                                                                                  Human; mouse; rat; splice transcript; detection; RNA transc
splice variant; transcriptome; oligonucleotide library; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Faigler S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental-specific genes
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                                                                                                                                                                                                                                                                                                                              20-JUL-2001; 2001WO-IB01903
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shoshan A, Wasserman A,
                                                                                                                                                                                                                                                                                                                                                                                                                              (COMP-) COMPUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-257383/30.
                                                                                                                                                                                                                                                  WO200210449-A2.
                                                                                                                                                                                                               Homo sapiens.
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AAS68767 standard; cDNA; 1774 BP.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity
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                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #5961.
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                                                                                   AAS70157 standard; cDNA; 1512 BP.
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                                                                                                                                                                                                (first entry)
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P-PSDB; ABG05970.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                               RESULT 12
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RESULT 13

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The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The carbon comparing expressed sequence tags for identifying expressed enes. (I) is useful in gene therapy techniques for restore normal activity of (II) or to treat disease states involving cuantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capposible for genetic disorders or other traits to assess bioldiversity canno acid sequences. AAS44197-AAS94564 represent novel human cald sequences at a five invention.

Specification, but was obtained in electronic format directly from WIPO
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100.0%; Pred. No. 5e-05;
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                                                           DNA encoding novel human diagnostic protein #4571.
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13-FEB-2002 (first entry)
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nes 32; Conserv
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   The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving cuantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical classing of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in dispnostics, forensics, gene mapping, identification of mutations cresponsible for genefic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and advanced to the contract of the polypeptide of descriptions in the polypeptide and polynucleotide and products dependent on DNA and advanced to the contract of the polypeptide and products dependent on DNA and the product of the products dependent on DNA and the product of the pr
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                 novel human diagnostic protein #26723.
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Pred. No.
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100.0%; Pre-
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                                                (first entry)
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Best Local Similarity
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                                                                                                                                                                     Homo sapiens.
                                                                                  DNA encoding
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              AAS90919;
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AC AAD36
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                                                                                                                                    Human; cytostatic; antisense gene therapy; screening; protein kinase;
cancer; liver; colon; tumour; inflammation; arthritic synovium; CAMK-X1;
calmodulin kinase; enzyme; RACE; rapid amplification of cDNA end; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing cancer, comprises determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase or upregulation of expression of the protein kinase, in the cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           two cells. The present sequence is 5' rapid amplification of cDNA ends (RACE) PCR primer used for constructing human calmodulin kinase CAMK-X1
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human. Homo saplens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. DNA Sequence 3 from Patent W00224947. AX399682 AX399682.1 GI:21335455 RESULT 1
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KEYWORDS
SOURCE
ORGANISM

PAT 06-JUN-2002

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ALIGNMENTS

Delaney, A.D. and Yoganathan, T. Cancer associated protein kinases and their uses Patent: WO 0224947-A 3 28-MAR-2002; REFERENCE AUTHORS TITLE JOURNAL

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BC032787.1 GI:21619664
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (06-UNN-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Contact: MGC help desk
Enail: gapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
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/translation="MorkeeddcsswkkQttnirktfifmevlgsgafsevflykQrl
TGKLFALKCIKKSPAFRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYIVMQLVSG
GELFPRILERGYYTEKDASLVIQQVLSAVKTIHENGIYHRDLKPENLLYLTPEENSKI
MYTDFGLSKWEQNGITMEGGTPGTPGYPFEVLAQVPEVLAQVEXIGVITYILLGYPP
RYTEFESKLFRRIKEGYFFESPFEPFMDISESAKDFICHLLEKDPNERYTCEKALSHPM
IDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNLHSFGVRPEVE
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VNGSLHISSSLVPMHQGSLAAGPCGCCSSCLNIGSKGKSSYCSEPTLLKKANKKQNFK
SEVMVPVKASGSSHCRAGQTGVCLIM"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14196444.
Contact: nisc_mgc@nhgilinin.gov,
Akhter,N. Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Bakealey,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Malker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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/lab_host="DH108"
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100.0%; Pred. No. 0;
iive 0; Mismatches
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/db_xref="LocusID:57172"
/db_xref="taxon:9606"
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                       CTICCAAACCTGGTGTCTATCCGGCAGAGGAGGAAGGCAGAGCAAGTGGAGCAGGGCTT
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KEYNORDS oligo capping; fis (full insert sequence). SOURCE Homo sapiens fetal brain cDNA to mRNA, clone_lib:FEBRA2 clone=FEBRA2007534. ORGANISM Homo sapiens ENKAryotes, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	REFERENCE AUTHORS Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hirao, M., Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanabe, T., Ozaki, K., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawal-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,	Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. TITLE NEDO human cDNA sequencing project JOURNAL Unpublished REFERENCE 2 (bases 1 to 2612) AUTHORS Isogai, T. and Yamamoto, J. TITLE NEDO PLOSA TARAO ISOGAI, T. AND TARAO ISOGA	Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mall:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' - & 3' - end one pass sequencing: RAB, HRI, and Biotechnology Center, Mational Institute of Technology and	Evaluation; clone selection for full insert sequencing: HRI and RAB. FEATURES 1. 2612 1. 2612 7/organism="Homo sapiens" 7/tissue_type="haraon:966" 7/tissue_type="haraon:966" 7/tissue_type="haraon:946" 7/tissue_type="haraon:946"	/clone_lib="FEBRAZ" /dev_stage="fetal" /note="cloning vector: pME18SFL3" BASE COUNT 619 a 750 c 645 g 598 t	Query Match 87.6%; Score 2143; DB 9; Length 2612; Best Local Similarity 99.8%; Pred. No. 0; Matches 2393; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	QY 39 GGCATCCTCAGAAGCTTCAGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAG 98	Qy 99 TTCCTGGAAGAACAGCACCACCAACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGG 158	OY 159 ATCAGGAGCTTTCTCAGAAGTTTTCCTGGTGAAGCAAGACTGACT	OY 219 TCTGAAGTGCATCAAGAAGTCACCTGCGGGACAGCAGCAGGAGAATGAGATTGC 278	OY 279 TGTGTTGAAAAAGATCAAGCATGAAAACATTGTGACCCTGGAGGACATCTATGAGAGCAC 338	QY 339 CACCCACTACTACCTGGTCATGCTGTTGTTGGTGGGGGGCTCTTTGACCGGATCCT 398	Qy 399 GGAGCGGGTGTCTACACAGAGAAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGC 458

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Homo sapiens calcium/calmodulin-dependent protein kinase I gamma (CAMKIG) mRNA, complete cds.
AF428261.1 GI:16755791
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2464)
Schutte, B.C., Bjork, B.C., Coppage, K.B., Malik, M.I., Gregory, S.G., Scott, D.J., Brentzell, L.M., Watanabe, Y., Dixon, M.J. and Murray, J.C.
A preliminary gene map for the Van der Woude syndrome critical region derived from 900 kb of genomic sequence at 1q32-q41
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Bjork, B.C., Watanabe, Y., Murray, J.C.
Characterization of the human orthol
(CamKig) at 1432-441
Unpublished
3 (bases 1 to 2464)
Bjork, B.C., Watanabe, Y., Murray, J.C.
Direct Submission
Submitted (05-0CT-2001) Genetics, Un
Iowa City, IA 52242, USA
Location/Qualifiers
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qq	Qy Db	Qy Db	O _Y	Qy Db	Oy Dp	Q _Y	QY	Qy Dp	Qy Db	Qy	Qy Db	Oy Db	Qy Dp	Oy Dp	O _Y	Qy Db	Qy Dp	Οy

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                                                                                                                                                                                                                      Direct Submission
Submitted (21-APR-1999) E-mail contact: humquery@sanger.ac.uk
Submitted (21-APR-1999) E-mail contact: humquery@sanger.ac.uk
Fils sequence was generated from cDNA clones isolated using
sequence from the bacterial clone 272L16 (AL02354) and EST
aguence from the bacterial clone 272L16 (AL02354) and identity of least 95% between the coordinates shown.
Further information can be found at
http://www.sanger.ac.uk/HGP/Chrl/ Partial, experimentally
determined gene.
Sanger Centre name: dJ272L16.Cl.1.
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1738)
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/note="matches EST AI215131 from clone IMAGE:1925595"
764. .842
HS272L161 1738 bp mRNA linear PRI 21-AP! Human gene isolated from PAC 272L16, chromosome 1, similar to calcium/calmodulin dependent protein kinases.
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1356. :1483
/number=11
join(1469. :1550,1553. :1723,1721. :1738)
//note="matches EST R05661 from clone 29500"
1484. :1736
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/note="matches EST AA351937"
931. .1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1432.1-32.3"
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653. .777
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Human DNA sequence from clone 272L16 on chromosome 1q32.1-32.3.
Contains the 3' end of the LaMB3 gene for Laminin, Beta 3' (Nicein, Ralinin, BM600) and a novel Rat Ca2+/Calmodulin dependent Protein Rinase LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D1S491 and a ca repeat polymorphism, complete sequence.
AL023754
AL023754.1 G1:4007152
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Submitted (27 NOV-1998) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
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Protein Kinase; D1S491; Kalinin; LAMB3; Laminin Beta 3; Nicein.
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   ACAGGCCGCCTGAAACTCAAGCCTCAGAAACCTCTAGACCCAGGTCCCCTGAGATCACAA
                                                                  TCACCGAGGCACCTGTCCTGGACCACAGTGTAGCACTCCCTGCCCTGACCCAATTACCCT
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Homo sapiens
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences such only a small overlap as described above.

This sequence is the entire insert of clone 272L16. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats all sequencing problems, such as annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                Cature key.

272116 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further Cancer Institute by the group of Pieter de Jong. For further details see http://Dacpac.med.buffalo.edu/ VECTOR: pCYPRC2 This sequence was generated from a human chromosome 1 bacterial clone config constructed in collaboration by the Sanger Centre chromosome I mapping group and Brian Schutte, Bryan Bjork, Kevin Coppage and Jeffrey Murray. Department of Pediatrics, University of Iowa, USA. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1.
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3020. .8067
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8380. .9083
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/note="LTR7 repeat: matches 1. .450 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                matches 1. .426 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4089. .5338
/note="MLT1A2-internal repeat: matches 358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5536. 5966
/note="MLT1A1-internal repeat: matches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jbb. .10/8
/note="MLT11 repeat: matches 281. .410 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="AluJo repeat: matches 101. .302 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460. .6781 'note="MLT1A1 repeat: matches 1. .318 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .711 of
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/note="MLT1A1 repeat: matches 318.
6020. .6459
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10929. .11005
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8150. .8293
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/note="MIR repeat: matches 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1082 .1506 /note="MSTD repeat: mat 1585 .1875 /note="MLTIA1 repeat: mat 1898 .2024
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/note="MER34 repeat: 0.3090. .3417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="q32.1-32.3"
/clone="RP1-272L16"
/clone_lib="RPCI-1"
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at: matches 26712748 of consensus" es 2 mer ca 84% conserved"	<pre>is 4 mer acac 86% conserved" repeat: matches 20186 of consensus"</pre>	eat: matches 80191 of consensus" 6313979)	3 AQ075457 AQ076848"	matches 60105 of consensus: matches 112249 of consensu	at: matches 21272750 of consensus"	epeat: matches 2189 of consensus"	matches 17422 of consensus	eat: matches 7262 of consensus" at: matches 26942749 of consensus"	at: matches 26412750 of consensus"	epeat: matches 4189 of consensus"	at: matches 23092748 of consensus"	eat: matches 63. ,140 of consensus"	epeat: matches 510538 of consensus"	epeat: matches 413543 of consensus"	epeat: matches 454503 of consensus"	repeat: matches 2366 of consensus"	epeat: matches 6172 of consensus"	eat: matches 1	2 mer ag 79% conserved"	: matches 1112 of consensus"	epeat: matches 30. 171 of consensus" eat: matches 26. 145 of consensus"	: matches 13259 of	at: matches 68541 o	repeat: matches 1503 of consensus"	epeat: matches 168 of consensus"	at: matches 22922723 of consensus"	es 2 mer ca 100% conserved"	es 4 mer caca 100% conserved"	peat: matches 4163 of consensus"	peat: matches 141355 of consensus"	
: mat 2 me	'9 copies 4 mer .12855 MER91A repeat:	eat: mat	ch: GSSs 279			repeat:	L2 repeat:	="MIR repeat: . 17953 ="L2 repeat: m	eat:	MER5A repeat:		".mir repeat:	MER34 repeat:	MER34 repeat: .20388	"LTR29 repeat: .20809	"MER47A repeat:	"MER34 repeat: .22278	="MLT1C repeat:22528	"26 copies 2 me	"MER81 repeat: .25034	-"MER5A repeat: 25193 -"MTR repeat: ma		repeat:	.26813 MER4A2 repeat:	885 1F repeat: 357	="L2 repeat:	927828 e="21 copies 2 927818	="10 copies 4	="HAL1 repeat: ma	="HAL1 repeat: ma 29820	4.
repeat_region repeat region	epeat_reg	repeat_region misc feature		t_regi	epeat_regi	repeat_region	epeat_regi	t_regi	֡֝֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֡֓֓֓֡֓֓֓֡֝֝֡֓֓֡֓֡֡֡֡֡֝֡֓֡֓֡֡֡֡֡֡	םר_ופטו	֓֞֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֡֓֓֓֓֓֡֓֓֡	cpedt_reg. epeat redi	t_regi	regi	epeat_req1	= , eat_reqi	epeat_regi	epeat_regi	repeat_region	repeat_region	repeat_region	repeat_region	epeat_regi	epeat_regi	epeat_r	chear—rear	red red	ereat redi	epeat redi	erecelica	

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30246. 30440 repeat: matches 7. .142 of consensus"
30246. 30440 repeat: matches 683. .874 of consensus"
30246. 30440 repeat: matches 683. .874 of consensus"
30239. 30788 repeat: matches 1189. .1455 of consensus"
30789. 31099
30789. 31090
30789. 31090
30789. 31067 consensus"
3100. 31167 repeat: matches 11.306 of consensus"
31170. 31914 repeat: matches 5448. .6190 of consensus"
31223. 32141
Anote="Linx repeat: matches 4317. .4530 of consensus"
32442. 33551
Anote="Linx repeat: matches 5. .426 of consensus"
32552. 33356
Anote="Linx repeat: matches 11.309 of consensus"
32552. 33356
Anote="Linx repeat: matches 11.309 of consensus"
33437. 33756
Anote="Linx repeat: matches 11.309 of consensus"
33437. 33756
Anote="Linx repeat: matches 11.309 of consensus"
3757. 36041
Anote="Charliela repeat: matches 11.1142 of consensus"
39293. 39437
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/note="MIR repeat: matches 1. .140 of consensus"

/note="match: 39584. .39839)

/note="match: GSS AQ070531"

/1165. .41445

/note="L2 repeat: matches 2180. .2489 of consensus"

41615. .41810
                   .618 of consensus"
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Pred. No. 0;
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29821. .30076
/note="HAL1 repeat: matches 355.
30095. .30228
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 41 Row: i Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
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                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (18-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Mus musculus, clone MGC:30513 IMAGE:4502479, mRNA, complete cds BC021840
BC021840.1 GI:18256866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MGC:30513 IMAGE:4502479"
/tissue_type="Eye, relina, mouse strain C57Bl\6"
/clone_lib=NHH MGC_94"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
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/protein_id="AAH21840.1"
/db_xref="GI:18256867"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
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100.0%; Pred. No. 9.2e-29;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                      Strausberg, R.
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Matches 71; Conserva
                                                                                                                                                        Mus musculus
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                                                                                                                                            Db 148276 GTTCCCTTTCTCCTTGAAAGTCCAGCACACTTCTTGTCTTCTCCCAGTTTCTCTG 148335
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                                                      Db 148036 CCTTAACTCCAGGATTAGCTCCCAAGTGCGCTGAGACCCAGCACCAGCACACTCTGGCCCT 148095
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                 2195 ATGAGTAAGGGCTGCAAGGAATTCTTATCCTGGCCACATGTCCTCCGTGCACACACCAA
                                                                                                                                                                                                                                                                                                                                                                              2255 IGGAGTTAACCTTGGAAGTTGACTATTTTAATGTCTGCCAGGAGTTCTAATCCTGCCTCT
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100.0%; Pred. No. 7.7e-33;
ive 0; Mismatches 0;
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Weston, M.D. and Kimberling, W.J.
A new polymorphism for the DLS70 locus
Unpublished (1993)
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/db_xref="taxon:9606"
/map="1941"
748. ,771
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dinucleotide repeat polymorphism.
Homo sapiens DNA.
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/rpt_type=tandem
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Direct Submission.

Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Numquery(Sanger.ac.uk Clone requests: clonerequest(Sanger.ac.uk)

On Jun 13, 2001 this sequence version replaced gi:13396595.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was contirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT: Tr:, TREMBL; WP: WORNDEP: Information on the WORNDEP.
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Mus musculus clone RP23-59N15, WORKING DRAFT SEQUENCE, 13 unordered
pieces.
                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 182054)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-106N23 is
from the RPCI-23 Mouse PAC Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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AC022675.3 GI:13940729
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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hes 0;
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Web site: http://mrcseq.har.mrc.ac.uk
Contact: mouseq@har.mrc.ac.uk
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44402 c 42300 g 46197 t
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/organism="Mus musculus"
/db_xref="taxon:10090"
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     AL365314.16 GI:14422218
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Best Local Similarity 100.0
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AL365314
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NRPPVSPAPPYSRPDSHDSSITEAPILDPSTPLPALTRLPCSHSRPSAPSGGRSLNC
LNGSLRISSSLVPMQQGPLATGCGCCSSCLNIGNRCKSSYCSEPTLFRKANKKQNF
KSEVAVPVRGGSTHFRGGQTGVCLVM* 1 others
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MITDFGLSKMEQNGVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPP
FYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALRHPW
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/translation="MGRKEEEDCSSWKKQTINIRKTF1FMEVLGSGAFSEVFLVKQRV
TGKLFALKCIKKSPAFRDSSLENEIAVLKRIKHENIVTLEDIYESTTHYYLVMQLVSG
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Bjork, B.C., Watanabe, Y., Murray, J.C. and Schutte, B.C.
Characterization of the human ortholog of rat CaM Kinase I gamma (CaMKig) at 1932-941
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                                                                                                    AF428262 2427 bp mRNA linear ROD 07-NOV-29
Mus musculus calcium/calmodulin-dependent protein kinase I gamma
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Bjork, B.C., Watanabe, Y., Murray, J.C. and Schutte, B.C.
Direct Submission
Submitted (15-0CT-2001) Genetics, University of Iowa, 140 EMRB, Iowa City, IA 52242, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 AACATTGTGACCCTGGAGGACATCTATGAGAGCACCACCACCACTACTACCTGGTCATGCAG 363
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/clone="TMAGE:4502479"
/clsue_type="retina"
/note="corresponds to EST BG293660"
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Local Similarity 100.0%; Pred. No. 9.2e-29;
Nes 71; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="1"
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                                                                                                                                                     Camklg) mRNA, complete cds
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86. .1519
                                                                                                                                                                                                     AF428262.1 GI:16755793
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                                                                                                                                                                                                                                                                Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 184754)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-59N15
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome
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Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone anne: 59_N_15
Center clone anne: 59_N_15
Center clone anne: 59_N_15
Center clone anne: 59_N_15
Sequencing vector: M13 M7815; 22$ of reads
Sequencing vector: M13 M7815; 22$ of reads
Sequencing vector: Plasmid: n/a: 78 of reads
Sequencing vector: Plasmid: n/a: 78 of reads
Sequencing vector: Plasmid: n/a: 78 of reads
Assembly program: Phrap; version 0.560731
Consensus quality: 19992 bases at least 040
Consensus quality: 181970 bases at least 040
Consensus quality: 181970 bases at least 020
Insert size: 182200; agarose-fp
Insert size: 18354; sum-of-contigs
Quality coverage: 12.9 in 020 bases; agarose-fp
Quality coverage: 12.9 in 020 bases; agarose-fp
outlity coverage: 12.9 in 020
* NOTE: Phis is a "verking draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* arbitrary: Gaps between the contigs are represented as
* trus of N, but the exact sizes of the gaps are unknown:
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (06-FBB-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAY 4, 2001 this sequence version replaced gi:7657723. All repeats were identified using RepeatMasker: Smit, A.F.A. 6 Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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4454: gap of 100 bp
5467: contig of 1013 bp in length
5567: gap of 100 bp
6717: contig of 1150 bp in length
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linear ROD 07-FEB-1999 partial cds.
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Protein Kinase.
Rattus norvegicus embryo (E18) brain cDNA to mRNA, clone_lib:S. Nakanishi clone:N5.
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                                                                                                                                                                                                                                                                                                                            57885 58084: gap of 100 bp 58085 141207: contig of 83123 bp in length 141208 144307: contig of 83123 bp in length 141208 184754: contig of 43447 bp in length. Location/Qualifiers 1. 184754 | /organism="Mus musculus" //db_xref="taxon:10090" //clone="RP23-59N15" //clone="RP23-59N15" //clone="lib="RPCI-23 Female Mouse BAC"
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                                                                               13893 13992: gap of 100 bp 13993 23297: contig of 9305 bp in length 23298 23397: gap of 100 bp 13929: contig of 15523 bp in length 38921 39020: gap of 100 bp 139020: gap of 100 bp 100 
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Pred. No. 1.7e-23;
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1268. 13892
/note="assembly_fragment"
1393. 23297
/note="assembly_fragment"
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9370. .11162
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/note="assembly_fragment"
5568. .6717
/note="assembly_fragment"
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/note="assembly_fragment"
8213. .9269
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/note="assembly_fragment"
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/note="assembly_fragment
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/note="assembly_fragment
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vector_side:left"
13892: cort
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                                                                                                                                                                                                                  Vokokura, H.
Direct Submission

Submitted (15-JUL-1996) Hisayuki Yokokura, Nagoya University School of Medicine, Department of Pharmacology; Tsurumai 65, Showa-ku, Nagoya, Alchi 466, Japan (Tel:052-744-2075, Fax:052-744-2083)

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TGKLFALKCIKKSPAFRDSSLENEIAVLKRIKHENIVTLEDIYESTTHYYLVWQLVSG
GELFDRILERGYYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKI
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FYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALRHPW
IDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFN"
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                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Sciurognathi; Muridae; Murinae;
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kinase I mRNA (L24907, L26288)"
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowle, S., Britava, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N. C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
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Yokokura, H., Terada,O., Naito,Y. and Hidaka,H.
Isolation and comparison of rat cDNAs encoding
Ca2+(calmodulin-dependent protein kinase I isoforms
Biochim. Biophys. Acta 1338 (1), 8-12 (1997)
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/db_xref="taxon:10116"
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/clone_lib="S. Nakanishi"
/dev_stage="embryo (E18)"
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Rattus norvegicus clone CH230-1D9,
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/protein_id="BAA19880.1"
/db_xref="GI:2077934"
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 76 contigs. The true order of the pieces

* is not known and thair order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley, K.C. Direct Submission Burnets Sequencing Center, Department Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 6, 2002 this sequence version replaced gi:21693754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 178272)
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Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus clone CH230-33NB, *** SEQUENCING IN PROGRESS ***, AC120477
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                      Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlson, E., Khan, U., King, L., Korvah, J., Kovar, C., Lozado, R., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Loulseged, H., Lozado, R.J., Lu, X., Lucier, R., Mari, J., Martinez, E., Massey, E., Mawhiney, E., Martin, R., Mari, M., Martinez, E., Massey, E., Mawhiney, E., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Ney, P., Ney, P., Moyen, N., Ney, P., Martinez, E., Worsen, M., Newtson, J., Okwonu, G., Oragunye, N., Oliedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Paul, L.L., Quiles, M., Ren, Y., Rives, M., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stenley, H., Stone, H., Sutton, A., Savetk, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Ward-Moore, S., Warren, R., Washington, C., Wang, S., Warten, R., Washington, C., Wang, S., Warren, R., Washington, C., Wang, S., Warren, R., Washington, C., Wang, S., Warren, R., Washington, C., Wallington, S., Weinstock, G. and Gibbs, R.
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NOTE: This is a 'working draft' sequence. It currently consists of 71 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (07-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 191584)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (132-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 18, 2002 this sequence version replaced gi:20522179.

Center: Baylor College of Medicine
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Worley, K.C.
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Search completed: March 15, 2003, 04:12:48
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1448)
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Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC014825 1448 bp mRNA linear ROD 07-AUG
Mus musculus, Similar to calclum/calmodulin-dependent protein
Kinase I, clone MGC:18933 IMAGE:3969343, mRNA, complete cds.
BC014825
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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YDENDAKLFEQILKAEYEFDSPYWDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWI
AGDFALDKNIHQSVSEQIKKNFAKSKWKQAFNATAVVRHMRKLQLGTSQEGQGGTGSH
GELLTPTAGGPAAGGCCRDCCVEPGSELPPAFPPSSRAMD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MPGAVEGPRWKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVAIKCIAKKALEGKEGSMENEIAVLHKIKHPNIVALDDIYESGGHLYLIMQLVSGGE
                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="Similar to calcium/calmodulin-dependent protein
kinase I"
                                                                                                                                                                                                           Gaps
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.3%; Score 32; DB 10; Length 1448; 100.0%; Pred. No. 4.4e-06; live 0; Mismatches 0; Indels
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/db_xrsf="taxon:10090"
/map="FVB/N"
/cmp="FVB/N"
/clone="MGC:18933 IMAGE:3969343"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     652 CCCTACAGCAAGGCTGTGGATTGCTGGTCCAT 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAH14825.1"
/db_xref="GI:15928726"
                                               identity to protein.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       .1244
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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March 15, 2003, 04:12:52 ; Search time 2223 Seconds
  (without alignments)
  3467.860 Million cell updates/sec
                                                                                                            US-09-960-643-2
2513
1 MGRKEEDDCSSWKKQTTNIR.....VKASGSSHCRAGQTGVCLIM 476
                                                                                                                                                                                                                                                                                                                                                 32308132
OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                     16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                           Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0 seq length: 2000000000
                                                                                                                                                                                           BLOSUM62
                                                                                                                                    Perfect score:
                                                                                                                                                                                           Scoring table:
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Maximum DB
                                                                                                                                                   Sequence:
                                       Run on:
                                                                                                                Title:
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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries Command line parameters:

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-UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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em_estin:*
em_estmu:*
em_estov:* em_estom:* em_estpl:*
em_estro:*
em_htc:*
gb_estl:* gb_est4:*
gb_est5:* gb_est2:* gb_htc:* em_estba:* gb_est3:* dp_gss:* EST: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		df			SUMMARIES		
Result No.	Score	Query	Length	DB	ID	Description	
1 2	1532			13	BM547443 BO934044	744	JRT
	17	50.0	808	· m		147	366
4.7	234		812	m		2	879
	117	46.1	1051	4		7 2	J.K.I.
7 0	11	•	740	m		8	355
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					ALIGNMENTS		
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DEFINITION		DURT	9	NIH	MGC_125 Homo	mkNA linear EST 20-FEB-Z sapiens cDNA clone IMAGE:5724	4450
ACCESSION	5', mJ	3 NA	edneuce				
VERSION KEYWORDS		143.	1 GI:18.	7812	13		
SOURCE	human	an. Sanjene	900				
	:	aryota; malia;	Eukaryota; Metazoa; Mammalia; Eutheria;		Chordata; Craniata; V Primates; Catarrhini;	ta; Vertebrata; Euteleostomi hini; Hominidae; Homo.	:
REFERENCE AUTHORS		1 (bases NIH-MGC ht	is 1 to 11 http://mg		≥		
TITLE		ional	Institutes o	es c	of Health, Mammalian	lian Gene Collection (MGC)	

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KEYWORDS
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                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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/incle="organ: ovary(pool of 3); Vector: 
                Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12713 row: 1 column: 19
High quality sequence stop: 623.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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AGENCORT_8802332 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6336727 BQ934044
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

( Dases 1 to 905)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   þe
                                                                                                                                                                         nPheAlaLysSerLysTrpArgGlnAlaPheAsnAlaAlaAlaAlaValValHisHisMetAr 318
MetileThrAspPheGlyLeuSerLysMetGluGlnAsnGlyIleMetSerThrAlaCys 180
                                                                                                                                                                                                                                                                                                                                                                                                                                       sAspProAsnGluArgTyrThr-CysGluLysAlaLeu---SerHisProTrpIleAspG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                gLysLeuHisMetAsnLeuHisSerProGlyValArgProGluVal---GluAsnArgPr 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M. A.G. E. Consortium (LLNL)
CNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
flound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.d column: 08
                                                                                                            GlyThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLysAlaVal
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/db_xref="taxon:10090"
/clone="IMAGE:6336727"
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Location/Qualifiers
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Euteleostomi;

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/note="Ostaling pooled brain, lung, testis; Vector:
/note="Ostaling pooled brain, lung, testis; Vector:
pcMv-SPORT6; Site_1: NotI; Site_2: EcoRv (destroyed); RNA
source anonymous pool of male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRv site is
elstroyed upon cloning). Average insert size 18 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
furber (Invitrogen). Research Genetics tracking code
021. Note: this is a NHLMGC Library."
                                                                     BI821474 809 bp mRNA linear EST 04-OCT-2001 603038366Fl NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5179336 5', mRNA sequence.
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 809)

Lu The Chitp://mgc.nci.nih.gov/.

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LibMalidy row: c column: 17

High quality sequence stop: 808.

I. 809

//clone='IlMAGE:SIP19336"

//clone='IlMAGE:SIP19336"

//clone='IlMAGE:SIP19336"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ArgAspSerSerLeuGluAsnGluIleAlaValLeuLysLysIleLysHisGluAsnIle
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/lab_host="DH10B"
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                                                                                                               BI821474
BI821474.1 GI:15933024
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/clone_lib="NIH_MGC_130"
//lb_host="DH10B (phage-resistant)"
//note="Organ: octocysts, Vector: pCMV-SPORT6.1.ccdb;
//note="Corgan: octocysts; Vector: pCMV-SPORT6.1.ccdb;
Primer: Oligo dT. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is
NIH_MGC Library.
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Mismatches:
Indels:
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Matches:
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Anote—"Organ: pooled lung and spleen; Vector: pCMV-SPORT6, Site_1: Not1: Site_2: EcoRV (destroyed); RNA source anonymous pool of Z4 week female lung, i6 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed proning). Average insert size 1.4 kb, insert size range 1-3 kb, Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NILMGC Library."
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 /lab_host="DH10B"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eu (Abasea I to 812)
I (Abasea I to 812)
IN INH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clond through the I.M.A.G.E. Consortium (LLNL)
Plate: LLAMI157 row: m column: 20
High quality sequence start: 2
High quality sequence start: 2
Location/Qualifiers
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                                                                                                         AspCysTrpSerIleGlyValIleThrTyrIleLeuLeuCysGlyTyrProPheTyr
                                        ValThrLeuGluAspIleTyrGluSerThrThrHisTyrTyrLeuValMetGlnLeuVal
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Matches:
Conservative:
Mismatches:
Indels:
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                                    Qγ
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                                                                                                            mRNA linear EST 05-MAR-2002 sapiens cDNA clone IMAGE:5732298
                                                                                                                                                                                                  Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                       L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs: remail.nih.gov
Email: cgapbs: remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium(LLNL)
DNA Sequencing Library Agency Column: 19
High quality sequence start: 11
High quality sequence stop: 651.
S Location/Qualifiers
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 105 ATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAGAACAGACCACCAACATCCGG 164
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Matches:
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Mismatches:
Indels:
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5732298"
/clone=1b="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
                                                                                                            BM807335
AGENCOURT_6575096 NIH_MGC_124 Homo
                                     AspProAsnGluArgTyrThrCysGluLys 270
                                                 (1-1129)
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1191.50
72.86%
70.60%
                                                                                                                                    5', mRNA sequence.
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AlaSerLeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIle 139
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AL560091 ALFL011_BC1 Homo sapiens cDNA clone CSODG002XN16 5 prime
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1051)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Fill-length cDNA libraries and normalization
Contact: Genoscope
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BP 191 91006 EVRY cedex - France
Emall: segref@enoscope.cns.fr, Web : www.genoscope.cns.fr.
_Locatlen/Qualifiers
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                                                                                                                                                                                                                                                                                                            /tissue_type="B cells from Burkitt lymphoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="cS0DG002XN16"
/clone_lib="LTI_FL011_BC1"
/sex="male"
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1158.00
84.29%
72.44%
                            mRNA sequence
                                                                                         Homo sapiens
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Best Local Similarity:
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Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi; Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 740)

2 (bases 1 to 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaValAspCysTrpSerIleGlyValIleThrTyrIleLeuLeuCysGlyTyrProPro 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      711 GCGTTGACTGCTGGTCCATCGGAGTGATTGCCTACATCTTGCTCTGCGGGTACCTCGSCT 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyAsnThralaLeuHisArgAspIleTyrProSerValSerLeuGlnIleGlnLysAsn 298
AlaCysGlyThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLys 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheTyrGluGluThrGluSerLysLeuPheGluLysIleLysGluGlyTyrTyrGluPhe 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5179957"
/clone_lib="NIH_MGC_115"
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Location/Qualifiers
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Percent Similarity:
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/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
pCWV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age for Library is
oligo-dT primed and directionally cloned (EcoRV site is
doligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
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Matches:
Conservative:
Mismatches:
Indels:
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730 GAAGAAACG 738
                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. I. (bases 1 to 1068)

In Indeplay to 1068)

In Institutes of Health, Mammalian Gene Collection (MGC)

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llh.gov

Plate: LLAM12788 row: b column: 19

High quality sequence stop: 592.
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Homo sapiens cDNA clone IMAGE:5753010
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Homo sapiens"
/db_xxef="taxon:9606"
/clone="Thanses:5753010"
/clone_lib="NIH_MGC_115"
/lab_host="DH108"
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BM921532.1 GI:19371911
EST.
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45.13%
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Best Local Similarity:
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1 (bases 1 to 742)

1 (bases 1 to 742)

2 National Institutes of Health, Mammalian Gene Collection (MGC)

2 Unpublished (1999)

3 Contact: Robert Strausberg, Ph.D.

5 Contact: Robert Strausberg, Ph.D.

5 Email: Gapbs-rémail.nih.gov

7 Tissue Procurement: Life Technologies, Inc.

5 CDNA Library Preparation: Life Technologies, Inc.
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Corganism="Homo sapiens"

Ab_xref="taxon: 9606"

Clone="IMAGE:5173587"

/clone="Image:5173587"

/lab_host="DHIBMG_115"

/lab_host="DHIBM"

/note="Organ: pooled brain, lung, testis; Vector:

/note="organ: pooled brain, lung, age range 23-27; lange lung, age 27; and 1 male testis, age 69. Library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI818261 742 bp mRNA linear EST 04-OCT-2001 603032510F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5173587 5',
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                                             MetileThraspPheGlyLeuSerLysMetGluGlnAsnGlyIleMetSerThr-AlaCy
Tourn constant of the high quality sequence stop: 742.

Location/Qualifiers
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AUTHORS
TITLE
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COMMENT
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B1753035 731 bp mRNA linear EST 25-SEP-2001 603025844F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5196323 5', mRNA sequence. B1753035
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oligo-dr primed and directionally cloned (BcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-960-643-2 (1-476) x BG293660 (1-818)
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TITLE
JOURNAL
COMMENT
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23.27 yo. Library is ollgo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NHMC Library."
                                                                                                                                                  Uppublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: agapsar Femail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
CLONE distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAMI491 row: g column: 12
High quality sequence stop: 729.
                                                Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 731)
NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Matches:
Conservative:
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/organism="Homo sapiens"
/db_xxef="taxon:9606"
/clone="InAGE:5196323"
/clone=lbb="NIH_MGC_114"
/lab_host="DH108"
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BI753035.1
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BG293660 818 bp mRNA linear EST 21-FEB-2001 602390529F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4502479 5',
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLAM10371 row: i column: 08
High quality sequence stop: 765.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 818)
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/tissue_type="retina"
/tasue_type="retina"
/tasu
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LeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIleValHis 141
                                                                                                                                                                             182 ThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLysAlaValAsp
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/db_xref="taxon:10090"
/clone="IMAGE:4502479"
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BG293660.1 GI:13053536
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NIH-WGC http://mgc.nci.nih.gov/.
NIH-WGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rfmail.nih.gov
Tissue Procurement: Millos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                   HisArgAspLeuLysProGluAsnLeuLeuTyrLeuThrProGluGluAsnSerLysIle 160
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                                                                  LysGlnArgLeuThrGlyLysLeuPheAlaLeuLysCysIleLysLysSerProAlaPhe
                                                                                                  ArgAspSerSerLeuGluAsnGluIleAlaValLeuLysLysIleLysHisGluAsnIle
                                 LysThrPhellePheMetGluValLeuGlySerGlyAlaPheSerGluValPheLeuVal
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BG715920.1 GI:13995107
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AUTHORS
TITLE
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/ Organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="INAGE:4799224"
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//lab_host="DH10B"
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Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnh.gov
Plate: LLAM10688 row: e column: 17
High quality sequence stop: 766.
Location/Qualifiers
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                                                                                                                         918 bp mRNA linear EST 21-AUG-2002
AGENCOURT_8744314 Lupski_sclatic_nerve Homo sapiens cDNA clone
BO949629
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NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Proturement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

thtp://image.libl.gov

plate: LLAM13629 row: g column: 20

High quality sequence stop: 697.
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 918)
                                      918
200
32
43
5
                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Lupski_sciatic_nerve"
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Mismatches:
Indels:
                                                                                        yrGluGluThrGluSerLysLeuPheGluLysIleLys 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
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Matches:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                ValSerGlyGlyGluLeuPheAspArgIleLeuGluArgGlyValTyrThrGluLysAsp 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaSerLeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIle 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValHisArgAspLeuLysProGluAsnLeuLeuTyrLeuThrProGluGluAsnSerLys 159
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                                      20
                                                                             21 LysThrPheIlePheMetGluValLeuGlySerGlyAlaPheSerGluValPheLeuVal 40
MetGlyargLysGluGluAspAspCysSerSerTrpLysLysGlnThrThrAsnIleArg
                                                                                                     41 LysGlnArgLeuThrGlyLysLeuPheAlaLeuLysCysIle --- LysLysSerProAla
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discovery

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CysGluLysAlaLeuSerHisProTrpIleAspGlyAsnThrAlaLeuHisArgAspIle 287
                                                                                           GluSerAlaLysAspPheIleCysHisLeuLeuGluLysAspProAsnGluArgTyrThr
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/
                                                                                                                                                                                     Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
                                                                                                            451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 IleThrTyrIleLeuLeuCysGlyTyrProProPheTyrGluGluThrGluSerLysLeu 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 PheGluLysIleLysGluGlyTyrTyrGluPheGluSerProPheTrpAspAspIleSer 247
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181
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                                                      Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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Matches:
Conservative:
Mismatches:
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       Genome_Res. 6 (9), 791-806 (1996)
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco Rv sites of the pcMvsporr 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
18 a 263 c 293 g 185 t 3 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 962)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr.
Location/Qualifiers
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GluArgGlyValTyrThrGluLysAspAlaSerLeuValIleGlnGlnValLeuSerAla 130
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Search completed: March 15, 2003, 06:39:01 Job time : 2231 secs



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Sequence 4, Application US/0993464
Publication No. US20030027153A1
GENERAL INFORMATION:
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Darker, Alexander
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILER REFERENCE: 3322/LH702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT APPLICATION NUMBER: US 09/757,300
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR SEQ ID NOS: 90
SOFTWARE: PatentIn version 3.0
 Sequence 6, Appli
Sequence 1, Appli
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11 US-09-935-464-48
10 US-09-935-466-13
10 US-09-935-466-13
10 US-09-937-825-1
10 US-09-937-826-1
10 US-09-937-826-1
10 US-09-937-832-1
11 US-09-938-842A-786
10 US-09-938-842A-794
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Conservative:
Mismatches:
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LENGTH: 1738
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    Score:
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-MODEL=frame+_pan.model._DEW=xlh
-Q-Zega2_1/USPTQ_spool/US09960643/runat_07032003_090518_19918/app_query.fasta_1.647
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-TRANS-human40.cdi -LIST-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100
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-MAXIN-2NORO000000 -USER=US099606643_GCGN_1_157_Crunat_07032003_090518_19918
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=0.5 -DELOP=6 -DELEXT=7
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 2, A
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
3: /cgn2_6/ptodata/2/pubpna/GC6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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                   GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                           nucleic search, using frame_plus_p2n model
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US-09-935-464-2
US-10-024-036B-1
US-10-024-036B-3
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Listing first 45 summaries
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Query DB:	Matc	ch:	100.00% 9	Indels: Gaps:	0 0	
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Oy Db	21	LysThrPhelleP 	.ePheMetGluValLeuG] 	uGlySerGlyAlaPheSe 	erGluValPheLeuVal 	40 137
Qy	41	LysGlnArgLeuThrC 	SlyLysLeuPhe	AlaLeuLysCysIleLy: 	/sLysSerProAlaPhe 	60 197
Qy Db	61 198	ArgAspSerSerLeuGl 	uAsnGluIl \GAATGAGAT	eAlaValLeuLysLysIle GCTGTGTTGAAAAGAT	leLysHisGluAsnile 	80 257
Qy Db	81 258	ValThrLeuGluA 	3luAspileTyrGluSerT} 	GluSerThrThrHisTyrTyrLe 	.euValMetGlnLeuVal 	100 317
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Oy Dp	121 378	SerLeuVallleG AGTCTGGTGATCC	GlnGlnValLeuSerA] 	lavallysTyrLeuHisG 	isGluAsnGlyIleVal 	140 437
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oy Pa	181 558	GlyThrProGlyTy 	yrValAlaProGluVal 	.LeuAlaGlnLysE scTGGCCCAGAAAC	roTyrSerLysAlaVal 	200
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Oy Dp	221 678	GluGluThrGluSe	serLysLeuPheGluLysIle 	LysGluGlyT 	yrTyrGluPheGluSer 	240 737
Oy Dp	241	ProPheTrpAspAs 	pileSerGlu8 	SeralaLysAspPhelleCy 	ysHisLeuLeuGluLys GCCACTTGCTTGAGAAG	260 797
Qy Dp	261 798	AspProAsnGluA 	oAsnGluArgTyrThrCysGluLysAla 	ysAlaLeuSerHisPro 	otrpileAspGly	280 857
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Oy Db	301 918	LysSerLysTrpArg 	rgGlnAlaPheAsnAlaAla 	AlavalvalH GCTGTGGTGC	isHisMetArgLysLeu 	320 977
Qy Db	321 978	HisMetAsnLeuHisSerP 	isSerProGlyValArg ACAGCCCGGGCGTCCGC	JProGluValG 	luasnargProProGluThr 	340 1037

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APPLICANT: Meyer, Joanne
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrangton-Martin, Rory
APPLICANT: Barker, Alexander
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/JH702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT APPLICATION NUMBER: US 09/757,300
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR PILING DATE: 2001-08-23
PRIOR PILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Version 3.0
SEQ ID NO 2
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Matches:
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US-09-935-464-2
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                                                                 APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: 68730 and 69112, Protein Kinase
TITLE OF INVENTION: Molecules and Uses Therefor
FILE REFERENCE: MPI2000-531P1R(M)
CURRENT APPLICATION NUMBER: US/10/024,036B
CURRENT FILING DATE: 2001-12-17
PRIOR FILING DATE: 2000-12-22
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Matches:
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RESULT 3
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Sequence 1, Application US/10024036B;
Publication No. US20030028004A1;
GENERAL INFORMATION:
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UMBER: US/10/024,036B
2001-12-17
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Patent No. US200200774581

GENERAL INFORMATION:

APPLICANT: Ni et al.

TITLE OF INVENTION: Antibodies

FILE REFERENCE: PTO18P1

CURRENT FILING DATE: 2001-04-17

PRIOR APPLICATION NUMBER: PCT/US0/28666

PRIOR PELICATION NUMBER: 60/16/35, 788A

CURRENT APPLICATION NUMBER: PCT/US0/28666

PRIOR PELICATION NUMBER: 60/16/35, 885

PRIOR PELICATION NUMBER: 60/16/3, 246

PRIOR PLING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: 60/16/2, 246

PRIOR PLING DATE: 1999-11-24

NUMBER OF SEQ ID NOS: 24

SOFTWARR: PATENTIN VET. 2.0

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Sequence 1, Application US/09817181

Sequence 1, Application US/09817181

Sequence 1, Application US/09817181

Sequence 1, Application US/09817181

SEQUENCE 1 INFORMATION: ACID OF THE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREVER ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREVER INVENTION: AND USES INVENTION: AND USE INVENTION: AND USES INVENTION: AND USE INVENTION: AND USES INVENTION: AND USES INVENTION: AND USES INVENTION: AND USE INVENTION: 
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ORGANISM: Human
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APPLICANT: MONTALING MARTIN, ROLY
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APPLICANT: Barrington-Martin, Rory
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APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Darker Alexander
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REPERENCE: 3322/1H702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
NUMBER OF SEQ ID NOS: 90
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                                                                                              GluLysAspProAsnGluArgTyrThrCysGluLysAlaLeuSerHisProTrpIleAsp
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; Publication No. US20030027153Al
; GENERAL INFORMATION:
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Qy 272 LeuSerHisProTrp-IleAspGlyAsnThrAlaLeuHisArgAspIleTyrProSerVa 291 	
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Qy 291 ISerLeuGlnIleGlnLysAsnPheAlaLysSerLysTrpArg 305 	QY 447447 Db 147048 CCTCTGTGCTTTGCAGAAGGAAGTGTAGGGGGGCTTGGTTATCTTTATCTTTTCTGCAGG 147107
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146028 AGGGGTGGGAAAGCTGTTCTGGGCCCCTGGAGGCTGGGCTGGCAGGGGCTGACATAAGG	447
09 303 303 303 303 303 303 303 303 303 3	Db 147168 CTACCACCTCTGCCCTGCCCCATCGACTCTTCCTTCCTCAAATACTTCAAAGGTTGTTGC 147227
305	Qy 448AsnPheLysSerGluvalMetValProvalLysAlaSerGlyS 462
Db 146148 GTGGGCACCCAGGTTTCAAGAGGCCACAAGGGAAAGGGAAAGTTTAAGCTCCAAGGCCCT 146207 Qy 306	462
14	288
Qy 311 aalavalvalHisHisMetargLysLeuHisMetasnLeuHisSerProGlyValargPr 331	RESULT 8 US-09-35-464-46 ; Sequence 46, Application US/09935464 ; Publication No. US20030027153A1
	GENERAL INFORMATION: APPLICANT: Mayer, Joanne APPLICANT: Barrington-Martin, Rory APPLICANT: Parker, Alexander
OGlullethrilethrGlualaProValLeuAspHisSerValAlaLeuProAlaLeuth 37 	; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSY; TITLE OF INVENTION: DISONDERS SUCH AS SCHIZOPHRENIA; FILE REFERENCE: 3322/14702 USI; CURRENT APPLICATION UMBER: US/09/935,464
Qy 371 rGlnLeuProCysGlnHisGlyArgArgProThrAlaProGlyGlyArgSerLeuAsnCy 391 	CURRENT FILING DATE: 2001- PRIOR APPLICATION NUMBER: U PRIOR FILING DATE: 2001-01- NUMBER OF SEQ ID NOS: 90
Oy 391 sLeuValAsnGlySerLeuHisIleSerSerSerLeuValProMetHisGlnGlySerLe 411	w
Oy 411 ualaaladiyProCysGlyCysCysSerSerCysLeuAsnIleGlySerLysGlyLysSe 431) ORGANISM: Homo sapiens) FEATURE: NAME/KEY: misc_feature OTHER INFORMATION: n=a or g or c or t/u
Qy 431 rSerTyrCysSerGluProThrLeuLeuLysLysAlaAsnLysLysGln 447 	Length:
44	e: 760.00 Matches: 1 on 100.00% Conservative: 0
Db 146688 AGCCAAAAGATGGAGCCCCAGCTTGGGTCTGAAAGAAATCGGTCAACAGGACTGAAAGAAA	
447	US-09-960-643-2 (1-476) x US-09-935-464-46 (1-480)
DD 146748 TGGACACAAAGGCCTCTCCCACTCATAGGCAGCATATATAGGGAGGG	Qy 1 MetGlyArgLysGluGluAspAspCysSerTerpLysLysGlnThrThrAsnIleArg 20
146	Db 30 ATGGTTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAACAGACCACCAACATCCGG 89
Qy 447 447	90 AAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAGTTTTCCTGGTG

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                                                                          ValThrLeuGluAspIleTyrGluSerThrThrHisTyrTyrLeuValMetGLnLeuVal 100
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|TGTGAAATCTTCCGGGCCAAGGACAAGACGACAGGCAAGGTGCACACCTGCAAGAAGTTC 165
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150 AAGCAAAGACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCACCTGCCTTC
                                          15 GlnThrThrAsnIleArgLysThrPheIlePheMetGluValLeuGlySerGlyAlaPhe
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                                 ArgAspSerSerLeuGluAsnGluIleAlaValLeuLysLysIleLysHisGluAsnIle
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APPLICANT: Olandt, Peter J.
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
FILE REFERENCE: 10448 017001
CURRENT APPLICATION NUMBER: US/09/797,039
CURRENT FILING DATE: 2001-02-28
PRIOR PAPLICATION NUMBER: US 60/186,061
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 13
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Matches:
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                                                        MetGluGlnAsnGlyIleMetSerThrAlaCysGlyThrProGlyTyrValAlaProGlu
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LeuTyrLeuThrProGluGluAsnSerLysIleMetIleThrAspPheGlyLeuSerLys
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                                      LeuGluArgGlyValTyrThrGluLysAspAlaSerLeuValIleGlnGlnValLeuSer
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                                                                                                                                          GENERAL INFORMATION:
APPLICANT: 0landt, Peter J.
APPLICANT: 10 0landt, Peter J.
APPLICANT: Rapeller-Libermann, Rosana
TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
TITLE OF INVENTION: KINABE FAMILY MEMBERS AND USES THEREFOR
FILE REFERENCE: 10448-017001
CURRENT APPLICATION NUMBER: US/09/797, 039
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/186,061
PRIOR FILING DATE: 2000-02-29
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                     Sequence 1, Application US/09797039 Patent No. US20020042099A1
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NAME/KEY: misc_feature
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Best Local Similarity:
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GTTTACTACAACCGGCTGAAGAACTCGAAGATTGTCATCAGTGACTTCCATCTGGCTAAG
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                                                           LeuTyrLeuThrProGluGluAsnSerLysIleMetIleThrAspPheGlyLeuSerLys
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                              GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al.

APPLICANT: YAN, Chunhua et al.

APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TILE REFERENCE: CL000612DIV

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 05/207,281

PRIOR APPLICATION NUMBER: 09/734,030

PRIOR FILING DATE: 2000-15-30

PRIOR APPLICATION NUMBER: 09/734,030

PRIOR FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0
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Mismatches:
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            Sequence 1, Application US/10153921
Patent No. US20020142430A1
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747.50
54.91%
37.82%
29.75%
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ORGANISM: HOMO SAPIEN
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Best Local Similarity:
Query Match:
DB:
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  10-153-921-1
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Sequence 47, Application US/09935464
Publication No. US20030027153A1
GENERAL INFORMATION:
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYC,
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/14702 USI
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT APPLICATION NUMBER: US/09/935,464
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
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Publication No. US20020192204A1
GENERAL INFORMATION:
TITLE OF INVENTION: 15985, A NOVEL HUMAN SERINE/THREONINE
TITLE OF INVENTION: 159865, A NOVEL HUMAN SERINE/THREONINE
TITLE OF INVENTION: 10448-078001
CURRENT APPLICATION NUMBER: US/09/934,406
CURRENT PILING DATE: 2001-08-21
PRIOR PILING DATE: 2000-08-21
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Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version
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; LOCATION: (208)...(2505)
US-09-934-406-1
                    NAME/KEY: misc_feature;
OTHER INFORMATION: n=a
US-09-935-464-48
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                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 ORGANISM: HOMO
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| Publication No. US20030027153A1
| GeneRaL INFORMATION:
| APPLICANT: Meyer, Joane
| APPLICANT: Barrington-Martin, Rory
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIP
| TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
| FILL REFERENCE: 3322/H702 US|
| CURRENT FILLING DATE: 2001-08-23
| PRIOR FILLING DATE: 2001-01-09
| NUMBER OF SEQ ID NOS: 90
| SOFTWARE: Patentin version 3.0
| SOFTWARE: Patentin version 3.0
| SERVIN 470
| TYPE: DNA
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Matches:
Conservative:
Mismatches:
Indels:
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        SOFTWARE: PatentIn version 3.0 SEQ ID NO 47
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OF SEQ ID NOS: 90
                                                                              NAME/KEY: misc_feature;
CTHER INFORMATION: n=a
US-09-935-464-47
                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                           TYPE: DNA
ORGANISM: HOMO
                                                                                                                                Alignment Scores:
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US-09-935-464-48
                                 LENGTH: 467
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PAPPLICANT: Galger, Alexander
APPLICANT: Galger, Alexander
APPLICANT: Galger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER,
TITLE OF INVENTION: COMPOSITIONS CORREST OF CORREST FILE PREPERROCE: 2077. 001200
CURRENT APPLICANTON NUMBER: GO/186, L26
PRIOR APPLICATION NUMBER: GO/190, 479
PRIOR PILING DATE: 2000-03-107
PRIOR PILING DATE: 2000-04-28
PRIOR PLILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-08-03
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                                                                                                                                                             ------TCAGTGGAGGAGTC 2391
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--LysLeuHisMetAsn 323
                                                                                                                         LeuHis------SerProGlyValArgProGluValGluAsnArgProPro 338
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309 AsnAlaAlaAlaValValHisHisMetArg-
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US-09-796-692-7777/c
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Matches:
Conservative:
Mismatches:
Indels:
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NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7777
LENGTH: 474
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                                                                   NAME/KEY: unsure
LCCATION: (10)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LCCATION: (19)
OTHER INFORMATION: n=A,T,C or G
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                                     TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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Best Local Similarity:
Query Match:
                                                                                                                                                  OTHER INFORMATION:
US-09-796-692-7777
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Search completed: March 15, 2003, 07:54:16 Job time : 161 secs

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APPLICANT: Bandman, Jennifer L.
APPLICANT: Corley, Nell C.
APPLICANT: Guegler, Karl G.
APPLICANT: Guegler, Karl G.
APPLICANT: Goll, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KIRASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                  US-08-338-057-1

US-08-55-38-057-1

US-09-55-38-051-1

US-09-57-82-8-1

US-09-27-82-8-1

US-09-28-016-1

US-09-28-016-1

US-09-29-385-4

US-09-28-016-10

US-09-28-016-10

US-09-28-016-10

US-09-27-8-016-10

US-09-27-8-016-10

US-09-27-006C-38-10

US-09-27-006C-38-10

US-08-57-006C-38-10

US-08-58-94-10

US-09-58-54-10

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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08878989 Patent No. 5885803 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
   USA
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Sequence 12, Appl
Sequence 2, Appli
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2280.908 Million cell updates/sec
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1: /cgn2_6/ptodatca1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodatca1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodatca1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodatca1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodatca1/ina/PGTVS_COMB.seq:*
6: /cgn2_6/ptodatca1/ina/Packfiles1.seq:*
                        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                          nucleic search, using frame_plus_p2n model
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US-09-272-796-12
US-08-773-030-1
US-08-775-568A-2
US-09-529-093A-1
US-09-76-694-3
US-09-198-468-16
US-08-198-468-16
US-09-188-551A-1
US-09-159-385-3
US-09-186-277-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441362 seqs, 153338381 residues
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Maximum Match 100%
Listing first 45 summaries
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2513
1 MGRKEEDDCSSWKKQTINIR.
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 GlnAsnGlyIleMetSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 191
                                                                                                                                                                                                                                                                                                                                                                           53 Cyslle---LysLysSerProAlaPheArgAspSerSerLeuGluAsnGluIleAlaVal 71
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Mismatches:
Indels:
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                                                                                                                                                                                            Length:
Matches:
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            PF-0321
                                                            INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 1282 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
REGISTRATION NUMBER: 36,749
         REFERENCE/DOCKET NUMBER: PF
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-0555
TELEFAX: 415-845-4165
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: IMMEDIATE SOURCE:

: LIBRARY: PROSNOS

: CLONE: 827431

US-08-878-989-12
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292 SerLeuGlnIleGlnLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsnAlaAla 311
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                                                                                                                                                                                                                                                                                   312 AlaValValHisHisMetArgLysLeuHisMetAsnLeuHisSerProGlyValArgPro 331
873 CTGAGGGCCAGCTATGAGTTTGACTNTCCTTTCTGGGATGACATCTCAGAATCAGGCAAA 932
                                        AspPhelleCysHisLeuLeuGluLysAspProAsnGluArgTyrThrCysGluLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bandman, Olga
APPLICANT: Bandman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Gall, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
WHERE OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS SOFTWARE: FASTEED for Windows Version 2.0 CURRENT APPLICATION DATE: CAPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREE: Inc. STREE: Inc. STREE: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF-0321 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/09272796 Patent No. 6207148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1282 base pairs
TYPE: nucletc acid
STRANDEDNES: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-845-4166
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CLONE: 827431
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APPLICANT: BEASLEY, Ellen M.
APPLICANT: MERKLOY, Gennady
APPLICANT: MERKLOY, Gennady
APPLICANT: KETCHUM, Karen A.
APPLICANT: KETCHUM, Karen A.
APPLICANT: MEI, Ming-Hui
APPLICANT: YAN, Chunhua
APPLICANT: YAN, Chunhua
APPLICANT: YAN, Chunhua
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOO612
CCHRENT APPLICATION NUMBER: US/09/734,030
CCHRENT FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrThrHisTyrTyrLeuValMetGlnLeuValSerGlyGlyGluLeuPheAspArgIle 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 CAGAAG-------CGGGACGCCGCAAGGTGCGGAAAGCTGCCAAGAACGAAGATA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuGluArgGlyValTyrThrGluLysAspAlaSerLeuValIleGlnGlnValLeuSer 129
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Mismatches:
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Matches:
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      1113 TIGTTCCTGCCCACATCCGGAAGCTG
                                                                                                                                   ; Sequence 1, Application US/09734030; Patent No. 6461846; GENERAL INFORMATION:
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                                                                           1152 GAGGGCGAG 1160
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Best Local Similarity:
Query Match:
DB:
                                              332 GluvalGlu 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 3124
                                                                                                        RESULT 3
US-09-734-030-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaValValHisHisMetArgLysLeuHisMetAsnLeuHisSerProGlyValArgPro 331
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                                                                                                                                                                                                                                                                                                                                                                          573 TCCTACCTGCACAGCCTGGGGATCGTGCACCGGGACCTCAAGCCCGAAAACCTCGTGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGAGGGCCAGCTATGAGTTTGAGTTTGTGGGATGACATCTCAGAATCAGGCAAA
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                                                                                                                                                                                                                                     AlaPheSerGluValPheLeuValLysGlnArgLeuThrGlyLysLeuPheAlaLeuLys
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Mismatches:
Indels:
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                                             Length:
Matches:
                                       1.29e-86
990.00
74.928
59.758
                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                             Alignment Scores:
Pred. No.:
US-09-272-796-12
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                                                                                                                                                                                                                                                                                                                                                                                          AlaLeuHisArgAspIleTyrProSerValSerLeuGlnIleGlnLysAsnPheAlaLys 301
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SETTACTACAACCGGCTGAAGAACTCGAAGATTGTCATCACTGCATCTGGCTAAG 723
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                                                                                                  ValLeuAlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleThr 209
                                                                                                                  MetGluGlnAsnGlyIleMetSerThrAlaCysGlyThrProGlyTyrValAlaProGlu
                                                                                                                                                            TyrIleLeuLeuCysGlyTyrProProPheTyrGluGluThrGlu-------
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Patent No. 5856463
GENERAL INFORMATION:
APPLICANT: Prydz, Hans Peter Blankenborg
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LeuSerLysMetGluGlnAsnGly-----IleMetSerThrAlaCysGlyThrPro 183
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            Disease
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150
72
123
59
                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz STREET: 600 South Avenue West
CITY: Westfield
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,568A
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Mismatches:
            Uses
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Matches:
APPLICANT: Brede, Gaute
TITLE OF INVENTION: PSKH-1 Ribozymes and
TITLE OF INVENTION: Treatment
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                                                                                                                                                                                                                                         CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FOLGY, Shawn P.
REFERENCE/DOCKET NUMBER: FOR:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
                                                                                                                                                                                                                                                                                                                  TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                2.33e-54
664.50
54.95%
37.13%
                                                                                                                                                                                                                                                                                                                                                           3471 base pairs
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STRANDEDNESS: double
                                    NUMBER OF SEQUENCES:
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Best Local Similarity:
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                                                                                                                 COUNTRY:
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DB:
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APPLICANT: UNTEN, Walter H.M.L.
APPLICANT: DARKEN, Walter H.M.L.
APPLICANT: BARKEN, Clare H.
APPLICANT: MCGOMAN, Clare H.
APPLICANT: BLASINA, Alessandra
TITLE OF INVENTION: Human Checkpoint Kinase, hCDS1, Compositions and Methods
FILE REPERBNCE: TSRI 649.0
CURRENT APPLICATION NUMBER: US/09/529,093A
CURRENT FILING DATE: 1998-10-21
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                   1057
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ATA---TCCCAGAACCTCCTTAAACGTGCCTCCTCGCGCTGCCAGAGCACCAAATCTGCC 1261
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                                                                                                                                                                                                        CTAGTGTGTCCAACTGGCCAAGGACTTCATTGACCGCTGCTGCTGACAGTGGACCTGGA
GlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLysAlaValAspCysTrp
                                                 SerIleGlyValIleThrTyrIleLeuLeuCysGlyTyrProProPheTyrGluGluThr
                                                                                                  GluSerLysLeuPheGluLysIleLysGluGlyTyrTyrGluPheGluSerProPheTrp
                                                                                                                                                       CGTACCCGGCTGTACCGGCAGATCCTCAGGGGCAAGTACAGTTACTCTGGGGAGCCCTGG
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Patent No. 6413755
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ATCACCAGTGGAAAATACAACTTCATTCCTGAAGTCTGGGCAGAAGTCTCAGAGAAGCT 1442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 ThrGluLysAspAlaSerLeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHis 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                       735 AAAACTCTTGGAAGTGGTGCCTGTGGAGAGGTAAAGCTGGCTTTCGAGAGAAACATGT
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|795 AAGAAAGTAGCCATAAAGATCATCAGCAAAAGGAAGTTTGCTATTGGTTCAGCAAGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 LysHisGluAsnIleValThrLeuGluAspIleTyrGluSerThrHisTyrTyrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 LysLeuPheAlaLeuLysCysIleLysLys------
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142
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131
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                3.17e-47
586.50
52.60%
36.98%
23.34%
2.0
                                                 TYPE: DNA ORGANISM: Homo sapiens FEATURE:
SOFTWARE: Patentin Ver. SEQ ID NO 1
                                                                                                 NAME/KEY: CDS
LOCATION: (66)..(1694)
                                                                                                                                                                                                                                     Similarity:
                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                    Alignment Scores:
                                 LENGTH: 1858
                                                                                                                                  US-09-529-093A-1
                                                                                                                                                                                                                                                   Query Match:
DB:
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                                                                                                                                                                                       Pred. No.:
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1569 GAA-----AATGAATCCACAGGTCTACCCCAGGTTCTAGCCCAGCCTTCTACTAGT 1619
                                                                                                                                                                                                                                        1620 CGAAAGCGGCCC------CGTGAAGGGGAAGCCGAGGGTGCCGAGACCACAAAG 1667
                                                                                                                                                                                                                                                                                              271 AlaLeuSerHisProTrpIleAspGlyAsnThrAlaLeuHisArgAspIleTyrProSer 290
                                                                                                291 ValSerLeuGlnIleGlnLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsnAla 310
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                                                                                                                                                                                                              ----ArgProGluValGluAsnArgProProGluThrGlnAlaSerGluThrSerArg
                                                                                                                                                      311 AlaAlaValValHisHisMetArgLysLeuHisMetAsnLeuHisSerProGlyVal---
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Matches:
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Mismatches:
Indels:
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Patent No. 6451538
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/746,694
CURRENT FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 49
FEBRUARE 1736
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578.50
60.28%
43.90%
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                                                                   GCCTTAAGACACCCGTGG----
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ORGANISM: Homo sapiens
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US-09-746-694-3
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Best Local Similarity:
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GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                          116 ThrGluLysAspAlaSerLeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHis 135
                                                                                                                                             GluAsnGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrLeuThrProGlu 155
                                                                                                                                                                                            GluAsnSerLysIleMetIleThrAspPheGlyLeuSerLys---MetGluGlnAsnGly 174
                                                                                                                                                                                                                                                                                                                                           212 LeuLeuCysGlyTyrProProPheTyrGlu---GluThrGluSerLysLeuPheGluLys 230
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                   841 AATCATCCTTGCATCATCAAGATTAAAAACTTTTTTGATGCA---GAAGATTATTATAT 897
                                                                LysHisGluAsnIleValThrLeuGluAspIleTyrGluSerThrThrHisTyrTyrLeu
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Mismatches:
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CURRENT APPLICATION NUMBER: US/09/800,960
CURRENT FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 4
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; Sequence 1, Application US/09800960
; Patent No. 6387677
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574.50
48.89%
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LENGTH: 2061
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US-09-960-643-2 (1-476) x US-09-800-960-1 (1-2061)

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17 ThrasnIleArgLysThrPheIlePheMetGluValLeuGlySerGlyAlaPheSerGlu	4 10 4			5 TyrthrGluLysaspalaSerLeuVallleGlnGlnValLeuSeralaValLySTyrLeu 	State	55 GluGluAsnSerLys1leMetIleThrAspPheGlyLeuSerLysMetGlu::::::::::::::::::::::::::::::::::::	172 GINASNGlyileMetSerThralaCysGlyThrProGlyTyrValalaProGluValleu 	192 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyVallleThrTyrIle :::	12 LeuLeuCysGlyTyrProProPheTyrGluGluThrGluSerIysLeuPheGluLysIle	232 LysGluGlyTyrTyrGluPheGluSerProPheTrpAspAspIleSerGluSerAlaLys 	252 AspPheIleCysHisLeuLeuGluLysAspProAsnGluArgTyrThrCysGluLysAla :::	272 LeuSerHisProTrpIleAspGlyAsnThrAlaLeuHisArgAspIleTyrProSerVal 	2 SerLeuGlnIleGlnLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsnAla :::::::::	311 AlaalaValValHisHisMetArgLysLeuHisMetAsnLeuHisSerProGlyValArg ::: :::	11 ProGluValGluAsnArgProProGluThrGlnAlaSerGluThrSer	47ArgproserSerProGluileThrileThrGlualaProValLeuAspHis
Η ,	Db 19 Qy 5 Db 25	Qy 75 Db 314	Qy 9 Db 37	Oy 11 Db 43	Qy 13 Db 49	Qy 15 Db 55	Qy 17. Db 61.	Oy 19	Qy 21 Db 73	Qy 23	Qy 29	Oy 27. Db 91.	Oy 299	Qy 3. Db 10.	Oy 333 Db 108	Oy 34'

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384 ProGlyGlyArgSerLeuAsnCysLeuValAsnGlySerLeuHisIleSerSerSerLeu 403
                                                                                                                                                   404 ValProMetHisGlnGlySerLeuAlaAlaGlyProCysGlyCysCysSerSerCysLeu 423
                                                                                                                                                                                                                            ---SerTyrCysSerGluProThrLeu 439
364 SerValAlaLeuProAlaLeuThrGlnLeuProCysGlnHisGlyArgArgProThrAla 383
                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-00-198-446B-16
Sequence 16, Application US/08198446B
Sequence 16, Application US/08198446B
Patent No. 567496
GENERAL INFORMATION:
APPLICANT: Hartwell, Leland H.
APPLICANT: Hartwell, Leland H.
APPLICANT: Groudine, Mark T.
TITLE OF INVENTION: Cell Cycle Checkpoint Genes
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
STREET: 1420 Fifth Ave., Suite 2800
STREET: MA
COUNTRY: USA
COUNTRY: USA
COMPUTER: IBM PC Compatible
OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
COMPUTER: PREBA-104 PATA:
APPLICATION NUMBER: US/08/198,446B
FILING DATE: 18-FBB-1994
CARSIFICATION: 18-FBB-1994
CARSIFICATION: 18-FBB-1994
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                                                                                                                                                                                                                                                                                                   440 LeuLysLysAlaAsnLysLysGlnAsnPheLysSer 451
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ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FHCR17537
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NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHCR.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-82-8100
TELEFAX: 206-224-0779
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2934 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA to mRNA
DESCRIPTION: yeast MEC2 cDNA
HYPOTHETICAL: NO
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                                                                                                                                                                                                                              424 AsnileGlySerLysGlyLysSer--
                                                                                                                1266 CCACCACAGAAG------
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TOPOLOGY: lin
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US-08-198-446B-16
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Score: Percent Best Lo Query M	Score: Percent Si Best Local Query Matc	ore: rcent Similarity: st Local Similarity: ery Match:	562.50 48.50% 33.55% 22.38%	Matches: Conservative: Mismatches: Indels: Gaps:	157 70 165 78 15	
us-0	096-6	-643-2 (1-476)	x US-08-198-446	6B-16 (1-2934)		
Qy	10	SerSerTrpLysL TCATCAATGGTGG	SerSerTrpLysLysGlnThrThrAsnIleArgLysThrPheIlePheMetGluVa TCATCAATGGTGGCCAACAAGAAGTATTTTAAGGATTTTTCGATTATTGACGAAGT	eargLysThrPhe TTTTAAGGATTTTTC	-IlePheMetGluVal GATTATTGACGAAGTG	28 1003
Oy Dp	29	LeuGlySerGlyA::: 	laPheSerGluValPh ::: CATTTGCCACAGTAAA	IELEUVAlLYSGlnAr 	LeuGlySerGlyAlaPheSerGluValPheLeuValLysGlnArgLeuThrGlyLysLeu :::	48 1063
δα	49	PheAlaLeuLysC	ysileLysLysSerPr	oAlaPheArgAsp	PheAlaLeuLysCysIleLysLysSerProAlaPheArgAspSerSerLeuGluAsn :::	,
3 2	68	GluileAlaVali	euLysLysIleLysHi	SGluAsnIleValTh		1123
qq	1124	GAGTTAGAAGTAT	TGCAAAAGCTCAATCA	TCCAAGGATAGTACG	ATTGAAAGGATTTTAT	1183
Qy Db	88 1184	GluSerThrThrH GAAGATACTGAGA	tsTyrTyrLeuValMe: GTTATTATAGGTGAI	tGlnLeuValSerGl :::	GluSerThrThrH\sTyrTyrLeuValMetGlnLeuValSerGlyGlyGluLeuPheAsp 	107 1243
yo d	1244	ArgileLeuGluA ::: mmgmgcmgcmc	rgGlyValTyrThrGl 	uLysAspAlaSerLe 	ArglleLeuGluArgGlyValTyrThrGluLysAspAlaSerLeuValIleGlnGlnVal ::: ::	127
Qy	128	LeuSerAlaValL	ysTyrLeuHisGluAs	nGlylleValHisAr	LeuSeralaValLysTyrLeuHisGluAsnClyIleValHisArgAspLeuLysProGlu	47
qq	1304	CTCACAGCAATAA	AATACATTCACTCTAT	GGGCATCAGCCATCG	TGACCTAAAGCCCGAT	1363
Oy Dp	148	AsnLeuLeuTyrL ::: AATATTCTTA	euThrProGluGluAs ::::::: :TrGAACAAGACGATCC	nSerLysIleMetIl ::: :TGTATTGGTAAAGAT	AsnLeuLeuTyrLeuThrProGluGluAsnSerLysIleMetIleThrAspPheGlyLeu ::: AATATTCTTATTGAACAAGACGATCCTGTATTGGTAAAGATAACCGACTTTGGTCTG	167 1420
, Q	168	SerLysMetGluG		tSerThrAlaCysGl	SerLysMetGluGlnAsnGlyIleMetSerThrAlaCysGlyThrProGlyTyrVal	9
9	147T	GCAAAAGTACAAG	GAAATGGGTCTTTTA	GAAAACCTTCTGTGG	CACTTTGGCATATGTG	1480
Qy Dp	187	AlaProGluValL 	euAlaGlnLys: :: !CAGAGGTAAAGATAC	ATCCGTATCTCCTGA	AlaProGluValLeuAlaGInLys	194 1540
Qy	195		ysAlaValAspCysTr CGTTAGTGGATATGTG	<pre>'pSerIleGlyValIl ' ::: 'GTCAATGGGATGTCT</pre>	ProTyrSerLysAlaValAspCysTrpSerIleGlyValIleThrTyrIleLeuLeu 	213 1600
οy	214	CysGlyTyrProP	roPheTyrGluGluTh	ırGluSerLysLeuPh	eGluLysIleLysGlu	33
අ	1601	ACGGCCACTTAC	 CTTTTAGTGGTAGCAC		ACGGCCACTTATAGTGGTACCACACAGGACCAATTATATATA	ف
λ 4	234	GlyTyrTyrGluP	GlyTyrTyrGluPheGluSerProPheTrpAsp-	PASPASPIleSe	heGluSerProPheTrpAspAsplleSerGluSerAlaLysAsp	52
3	0	GGCICAIAICAI	GAAGGCCCTCA	MGATTTCCGGATATC	TGAAGAAGCAAGAT	1/1/
Qy Dp	253 1718	PhelleCysHisL TTCATAGATTCAT	euLeuGluLysAspPr GTTACAGGTGGATCC	OASnGluArgTyrTh AAATAATAGGTCGAC	PhelleCysHisLeuLeuGluLysAspProAsnGluArgTyrThrCysGluLysAlaLeu 	272 1777
Oy	273	SerHisProTrpI	leAspGlyAsnThrAl	a-LeuHisArg	SerHisProTrp1leAspG1yAsnThrAla-LeuHisArg	85
g	1778	AATCATCCCTGGA	TCAAGATGAGTCCATT	GGGCTCACAATCATA	TGGTGATTTTTCACAA	1837
Oy Dp	286	ATATCCTTATCAC	AATCGTTGTCGCAGCA	I ASPI GABATTATTAGABAA	AspileTyrProServalSe	292
Qy	6	rLeuGlnIleGln	LysAsnPheAlaLysS	erLysTrpArgGlnA	rLeuGln11eGlnLysAsnPheAlaLysSerLysTrPArgGlnAlaPheAsnAlaAl	12

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-----AACAGGATCAGGAAGACCAAGATGGAAAAATTCAAGGATTTAAAATACCCGCA 2002
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                                                                                                                                                                                                                                                                                              392 uValAsnGlySerLeuHisIleSerSerSerLeuValProMetHisGlnGlySerLeuAl 412
                                                                                                                                                                                                                                                               ------ProProGluThrGlnAlaSerGluThrSerArgProSerSerProGluIl 353
                                                                                                                                                                                            2003 CACGCCCTATTCGATATACACACCCAAAAGCATTGAAGCAGAAACTAGAGAAAAA
                                                                                                                                                                                                                                                                                                                                                               353 eThrileThrGluAlaProValLeuAspHisSerValAlaLeuProAlaLeuThrGlnLe
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                                                                aValValHisHisMetArgLysLeuHisMet-------
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STREET: 1420 Fifth Ave., Suite 2800
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: WA
COUNTER: WA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,693
FILING DATE: WAY 18, 1994
APPLICATION NUMBER: PCT/US93/04458
FILING DATE: February 18, 1994
APPLICATION NUMBER: DCT/US93/04458
FILING DATE: MAY 12, 1993
APPLICATION NUMBER: US 07/884,426
FILING DATE: MAY 12, 1993
APPLICATION NUMBER: US 07/884,426
FILING DATE: MAY 12, 1993
APPLICATION NUMBER: US 07/884,426
FILING DATE: MAY 12, 1993
APPLICATION NUMBER: US 07/882,051
FILING DATE: MAY 12, 1993
APPLICATION NUMBER: US 07/882,051
FILING DATE: MAY 12, 1992
APPLICATION NUMBER: US 07/882,051
FILING DATE: MAY 12, 1992
APPLICATION NUMBER: US 07/882,051
FILING DATE: MAY 12, 1992
APPLICATION NUMBER: US 07/882,051
FILING DATE: MAY 12, 1992
APPLICATION NUMBER: US 07/882,051
FILING DATE: MAY 12, 1992
APPLICATION NUMBER: US 07/882,051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hartwell, Leland H.
APPLICANT: Weinert, Ted A.
APPLICANT: Plon, Sharon E.
APPLICANT: Plon, Sharon E.
APPLICANT: Groudine, Mark T.
ITILE OF INVENTION: Cell Cycle Checkpoint Genes NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFENCE/DOCKET NUMBER: FHCR110798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/08870693
Patent No. 5866338
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1838 ATATCCTTATCACAATCGTTGTCGCAGCAGAAATTATAGAAAATATGGACGATGCTCAA 1897
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                                                                                                              PhelleCysHisLeuLeuGluLysAspProAsnGluArgTyrThrCysGluLysAlaLeu 272
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                                             GlyTyrTyrGluPheGluSerProPheTrpAsp---AspIleSerGluSerAlaLysAsp
                                                                  --------AsplleTyrProSerValSe
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APPLICANT: LIVI, GEORGE P.
APPLICANT: MCLAUGHLIN, MEGAN M.
APPLICANT: YOUNG, PETER R.
TITLE OF INVENTION: METHODS OF THE IDENTIFICATION OF TITLE OF INVENTION: PHARMACEUTICALLY ACTIVE COMPOUNDS
                                                                                                                                                                                 273 SerHisProTrplleAspGlyAsnThrAla-LeuHisArg---
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GTTTTTAACTTTAAAACCATTGCCTGACAGCATTATTCAA---
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CURRENT APPLICATION NUMBER: US/09/142,551A
CURRENT APPLICATION NUMBER: US/09/142,551A
CURRENT FILING DATE: 1998-09-10
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1996-03-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1333
                                                                                                                                                                                                                                                                                                                                                                                      312 aValValHisHisMetArgLysLeuHisMet----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/09142551A; Patent No. 6218136
; GENERAL INFORMATION:
; APPLICANT: KUMAR, SANJAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2284 -----TGCTGT 2289
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
TELEFAX: 206-224-0779
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2934 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
DESCRIPTION: yeast MEC2 CDNA
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Best Local Similarity:
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                                                                                                                                                                                                                                                       LOCATION:
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                                                                                                                                               27 GluValLeuGlySerGlyAlaPheSerGluValPheLeuValLysGlnArgLeuThrGly
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                                                      Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                        US-09-960-643-2 (1-476) x US-09-142-551A-1 (1-1333)
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                                              Length:
                                           3.46e-43
542.50
52.02%
34.09%
ORGANISM: Homo sapiens
                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                 Alignment Scores:
           US-09-142-551A-1
                                              Pred. No.:
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                                                                 325 HisSerProGlyValArg-ProGluValGluAsnArgProProGluThrGlnAlaSer--
305 ArgGlnAlaPheAsnAlaAlaAlaValWiSHisMetArgLysLeuHisMetAsnLeu
                               GACGAAGTCAAGGAGGAGATGACCAGTGCCCACTATGCGGGTAGACTACGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: AKIRA, SHIZUO
APPLICANT: KAWAL, TARO
APPLICANT : KAWAL, TARO
APPLICANTION: DNA CODING FOR SERINE/THREONINE KINASE
FILE REFERENCE: PH-569
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CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: JP97/261589
EARLIER FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09159385 Patent No. 5958748 GENERAL INFORMATION:
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542.50
48.03%
34.72%
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US-09-159-385-3
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                          SerLeuVallleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIleVal
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ACCCAGTICCTCAAGCAGATCCTGGACGGCGTTCACTACCTGCACTCTAAGCGCATCGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGGCGGGGAGCTCTTTGACTTCCTGGCGGAGAAGAGTCGCTGACGGAGGACGAGGCC 441
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                     GENERAL INFORMATION:
APPLICANT: AKTRA, SHIZUO
APPLICANT: KAWAI, TARO
TITLE OF INVENTION:
FILE REPERENCE: 081356/0128
CURRENT APLICATION NUMBER: US/09/186,277
CURRENT FILING DATE: 1998-11-05
EARLIER APPLICATION NUMBER: US/09/186,277
CURRENT FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARR: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 2132
                                                                                                                                                                                                                                                                                                                    2132
159
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158
158
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                     Length:
Matches:
; Sequence 3, Application US/09186277; Patent No. 6171841
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542.50
48.03%
34.72%
21.59%
                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                         ; LOCATION: (94)..(1455)
US-09-186-277-3
                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                NAME/KEY: CDS
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                                                                                                                                 802 GACGAGGAGTACTTCAGCAACACCAGCGAGCTGGCCAAGGACTTCATTCGCCGGCTGCTC 861
682 GAGGCGGACATGTGGAGCATCGGTGTCATCACCTATATCCTCCTGAGCGGTGCATCCCCG 741
                                                                                                  259 GluLysAspProAsnGluArgTyrThrCysGluLysAlaLeuSerHisProTrpIleAsp
                                 PheTyrGluGluThrGluSerLysLeuPheGluLysIleLysGluGlyTyrTyrGluPhe
                                                                742 TICCTGGGCGAGACCAAGCAGGAGACGCTCACCAACATCTCAGCCGTGAACTACGACTTC
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ADDRESSEE: Akzo No. 5614195el Patent Department
STREET: 1300 Piccard Drive, Suite 206
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Patent No. 5614195
GENERAL INFORMATION:
APPLICANT: Tomley, Fiona M.
APPLICANT: Bunstead, Janene M.
APPLICANT: Bunstead, Janene M.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
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CITY: Rockville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: sporozoite cDNA cloned in Lambda ZAPII CLONE: Em70-1
                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-960-643-2 (1-476) x US-08-464-164-1 (1-1400)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                        APPLICATION NUMBER: US/08/464,164
FILING DATE: June 2, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE: sporozoite
                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 256-5200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
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537.50
57.70%
40.00%
21.39%
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Floppy disk
                                                                                                                                                                                                                                                                                          LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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Mon Mar 17 12:14:43 2003

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299 PheAlaLysSerLysTrpArgGlnAlaPheAsnAlaAlaAlaValValHisHisMetArg 318
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162 IleThrAspPheGlyLeuSer---LysMetGluGlnAsnGlyIleMetSerThrAlaCys 180
                                                                                                                                                                                                                                                             GGAGCAAATGAATTTGAAATTCTAAAGAAAGTCGAGAAAGGAAAATTCACCTTCGATTTA 645
                                                                                                                                                                                                                                                                                                 241 ProPheTrpAspAspIleSerGluSerAlaLysAspPheIleCysHisLeuLeuGluLys 260
                   261 AspProAsnGluArgTyrThrCysGluLysAlaLeuSerHisProTrpIleAspGlyAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 ThrAlaLeuHisArgAspIle----TyrProSerValSerLeuGlnIleGlnLysAsn
                                                                       GlyThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLysAlaVal
                                                                                                                                                AspCysTrpSerIleGlyValIleThrTyrIleLeuLeuCysGlyTyrProProPheTyr
                                                                                                                                                                                                                      GluGluThrGluSerLysLeuPheGluLysIleLysGluGlyTyrTyrGluPheGluSer
                                                                                                                                                                                                                                                                                                                       766 GATGTTACTGCTAAGGATAGTATTAATCTTCCTTCTTGAGAGTACTATA---CTTAAT
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tomley, Fiona M.
APPLICANT: Dunn, Paul P. J.
APPLICANT: Bunn, Paul B. J.
APPLICANT: Wermeulen, Anno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Organon Teknika Corporation
STREET: 1330 Piccard Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93.309078.9
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08338057
Patent No. 5795741
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Gormley, Mary E. REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
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STATE: Maryland
COUNTRY: U.S.A.
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                                                                                                                                                                              sporozoite cDNA cloned in Lambda ZAPII
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                       ORGANISM: Eimeria maxima
STRAIN: Houghton
DEVELOPMENTAL STAGE: sporozoite
                                                     MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                          1.14e-42
537.50
57.70%
40.00%
21.39%
1400 base pairs
                                                                                           FRAGMENT TYPE: C-terminal
             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                    1..1368
                                           linear
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Query Match:
                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                           ORIGINAL SOURCE:
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                                                                    HYPOTHETICAL:
ANTI-SENSE: N
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                                                                                                                                                                                                                       NAME/KEY:
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US-08-338-057-1
                                          TOPOLOGY:
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GATGTTACTGCTAAGGATAGTATTAATCTTCCTTCTTGAGAGTACTATA---CTTAAT 822
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ProPheTrpAspAspIleSerGluSerAlaLysAspPheIleCysHisLeuLeuGluLys 260
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MEDULUM TYPE: Floppy disk
MEDULUM TYPE: Floppy disk
COMPUTER: ELOPPY disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,416
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/464,164
FILING DATE:
TILNG DATE:
TILNG DATE:
TILNG DATE:
SECOMMUTICATION NUMBER: 34,409
TELECOMMUTICATION NUMBER: 34,409
TELECOMMUTICATION NUMBER: 34,409
TELECOMMUTICATION INFORMATION:
TELEPHONE: (301) 256-5200
INFORMATION FOR SEQ ID NO: 1:
SEGUENCE CHRAACTERISTICS:
LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDENESS: double
STRANDENESS: double
TYPE: AND TANDENESS: AND
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Sequence 1, Application US/08668416
Patent No. 15843720:
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LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
CLONE: Em70-1
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DEVELOPMENTAL STAGE: sporozoite
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MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
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|GGAGCAAATGAATTTGAAAGTTGAAGGAGGAAAAGTTCACCTTGATTTA
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                                                                                       Conservative:
Mismatches:
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                                                                              Matches:
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                                                            1.14e-42
537.50
57.70%
40.00%
21.39%
                                                                                          Percent Similarity:
Best Local Similarity:
. NAME/KEY:
; LOCATION:
US-08-668-416-1
                                                      Alignment Scores:
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823 ATCAGGCAGTICCAGGGTACACAGAAGCTTGCTGCTGCTGCTGTTGCTGTACATGGGGAGT 882 ф

319 LysLeuHisMetAsn 323 ||||||| 883 AAATTAACAACAAAT 897

Qy Db

Search completed: March 15, 2003, 07:51:43 Job time: 79 secs

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GenCore version 5.1.4_p5_4578
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- protein search, using sw model OM protein

March 14, 2003, 14:04:21 ; Search time 14 Seconds (without alignments) 1410.195 Million cell updates/sec Run on:

Perfect score:

US-09-960-643-2 2513 1 MGRKEEDDCSSWKKQTTNIR.....VKASGSSHCRAGQTGVCLIM 476 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	βţ	Q63450 rattus norv	Q14012 homo sapien	_	_	P13234 rattus norv	Q16566 homo sapien	•		Q9p7i2 schizosacch	O15075 homo sapien	.09jlm8 musculu	Q13554 homo sapien		Q9uqm7 homo sapien		Q9z265 mus musculu		٠.,	P22517 saccharomyc	P11798 mus musculu	-	P08413 rattus norv		Q13555 homo sapien	P27466 saccharomyc	Q923t9 mus musculu	P11730 rattus norv	O14408 metarhizium		Q06850 arabidopsis			P38622 saccharomyc
SUMMARIES	ID	KCC1_RAT	KCC1_HUMAN	KCC4_MOUSE	KMLC_DICDI	KCC4_RAT	KCC4_HUMAN	KCC1_EMENI	KPSH_HUMAN	KCC1_SCHPO	DCK1_HUMAN	DCK1_MOUSE	KCCB_HUMAN	DCK1_RAT	KCCA_HUMAN	KCCA_RAT	CHK2_MOUSE	KCCD_HUMAN	KCCD_RAT	KCC2_YEAST	KCCA_MOUSE	KCCB_MOUSE	KCCB_RAT	CHK2_HUMAN	KCCG_HUMAN	KCC1_YEAST	KCCG_MOUSE	KCCG_RAT	KCC1_METAN	SPK1_YEAST	CDP1_ARATH	CDPK_SOYBN	DAPK_HUMAN	RCK1_YEAST
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	Query Match Length	374	370	469	295	474	473	414	424	332	740	756	664	433	478	478	546	499	533	447	478	542	542	543	472	446	529	527	382	821	610	208	1431	512
쓩	Query Match	46.0	45.9	27.8	27.6	27.6	27.2	25.9	25.6	25.1	24.4	24.1	24.0	24.0	24.0	23.8	23.8	23.7	23.5	23.4	23.5	23.1	23.0	23.0	23.0	23.0	22.8	22.5	22.5	22.2	22.1	21.6	21.6	21.3
	Score	1155.5	1152.5	697.5	694.5	692.5	684	651	643.5	630	612	909	603.5	602.5	602	599	297	594.5	591.5	588	584	579.5	578.5	578.5	578	577.5	574	566.5	565.5	558	526.5	543.5	543.5	m
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EMBL; L24907; AAA19670.1; -. EMBL; L26288; AAA66944.1; -. PDB; 1A06; 08-APR-98.

	Q28824 bos taurus Q63531 rattus norv							
CDP2_ORYSA K6A1_HUMAN	KMLS_BOVIN K6A1_RAT	KMLS_RABIT	K6A1_MOUSE	CDP3_ORYSA	KMLS_CHICK	DUN1_YEAST	KMLS_HUMAN	CDP1_ORYSA
нн			I ~	-	7	7	Н	7
533	1176	1147	724	542	1906	513	1914	534
21.3	$21.1 \\ 21.1$	21.1	21.0	21.0	20.9	20.8	20.7	20.7
536	531 530.5	530	527	526.5	525	523	521	520
34	36	8 6 8 6	40	41	42	43	44	45

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                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (42 KDA ISOFORM).
STRAIN=Sprague-Dawley; TISSUE-Lung;
MEDLINE=95035115; PubMed=9948038;
Cho F.S., Phillips K.S., Poducki B., Weaver T.E.;
"Characterization of a rat cDNA clone encoding calclum/calmodulin-dependent protein kinase I.";
Biochim. Biophys. Acta 1224:156-160(1994).
                          KCC1_RAT STANDARD; PRT; 374 AA.
063450; 063084;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAX-2000 (Rel. 39, Last annotation update)
Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
(CAM kinase I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (37 KDA ISOFORM).
MEDLINE-94075341; PubMed-8253780;
Picciotto M.R., Czernik A.J., Nairn A.C.;
"Calcium/calmodulin-dependent protein kinase I. cDNA cloning and identification of autophosphorylation site.";
J. Biol. Chem. 268:26512-26521(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF SHORT FORM.
TISSUE=Brain;
MEDLINE-96182648; PubMed-8601311;
                                                                                                                                                                                                    NCBI_TaxID=10116;
RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 VLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMSTACGTPGYVAPE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 AAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVLDHSVALPA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTQLPCQHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCCSSCLNIGSKG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 WKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIN; 004998; ...
InterPro; IPR00019; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pram; PP00066; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00110; PROTEIN_KINASE_ST; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
PROSPHOTYLATION; ATP-binding; Alternative splicing.
PROSPHOTYLATE; PS0011; PROTEIN_KINASE.
PROMAIN 20 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 VLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISES
                                                                                                                                                                                                              SUBUNIT: MONOMER.
ILSUE SEPECIFICITY: UBLOUITOUS.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CALMODULIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 2e-65;
46; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
PHOSPHORYLATION (AUTO-).
K->A: LOSS OF ACTIVITY.
57FA20ECE00FA76C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.9%; Score 1152.5;
55.8%; Pred. No. 2e-6
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HSSP; Q63450; 1A06.
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nes 239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:1459; CAMK1.
MIM; 604998; -
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49
141 1
177 1
49
370 AA;
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NP_BIND
BINDING
ACT_SITE
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (AUTO-).
SQESQUARHGELLTPTAGGPAAGCCCRDCCVEPGSELP
PAPPPSSRAMD -> HQPGGTGTDS (IN 37 KDA
ISOFORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00107; PROTEIL_KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_ST; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
Transferase; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; Calmodulin-binding; Phosphorylation; APP-binding; APF-binding; APF-binding; APF-binding; APF-binding; APF-BINDING (BY SIMILARITY).
DOMAIN 287 321
ATP (BY SIMILARITY).
ACT_SITE 141 141 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 VKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMSTACGTPGYVAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 VLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISES
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type I (EC 2.7.1.123)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F -> G (IN REF. 1).
A -> R (IN REF. 1).
A -> R (IN REF. 1).
37889B3DEF033AB2 CRC64;
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Calcium/calmodulin-dependent protein kinase t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43; Mismatches
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Prodom; PP00069; pkinase; 1.
Brodom; PP0000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41638 MW;
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| ATAVVRHMRKLQLGTSQEG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 AAAVVHHMRKLHMNLHSPG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112
118
309
374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CAM kinase I).
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Q14012;
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MOD_RES
VARSPLIC
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KCC1_HUNAN

CCC1_HUNAN

CCC1_HUNAN

DT 15-JUL.

DT 15-JUL.

DT 15-JUL.

DT 16-OCT.

DE Calciu

DE CAMX 1.

GN CAMX 1.

MAMMALY

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Tan J.L., Spudich J.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Nati. Acad. Sci. U.S.A. 84:3038-3042(1987).
-!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
-!- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
                                                                                                               KCC4_MOUSE STANDARD; PRT; 469 AA.
P08414; Q61381;
01-AAG-1998 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calcium/calmodulin-dependent protein kinase type IV catalytic chain (EC 2.7.1.123) (CAM kinase-GR) (CAMK IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Screening an expression library with a ligand probe: isolation and sequence of a cDNA corresponding to a brain calmodulin-binding
------AAG-C-CCRDC-----
                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- TISSUE SPECIFICITY: BRAIN AND TESTIS.
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                      Hahn W.E.;
                                                                                                                                                                                                                                                                                                STRAIN=BALB/C; TISSUE-Brain;
MEDLINE=91372388; PubMed=1893997;
Jones D.A., Glod J., Wilson-Shaw D., Hahn W.E., Sikela J.M.;
"CDNA sequence and differential expression of the mouse
Ca2+/calmodulin-dependent protein kinase IV gene.";
FEBS Lett. 289:105-109(1991).
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89122027; PubMed-2536634;
Sikela J.M., Law M.L., Kao F.-T., Hartz J.A., Wei Q., I
"Chromosomal Localization of the human gene for brain
Ca2+/calmodulin-dependent protein kinase type IV.";
Genomics 4:21-27(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000719; Buk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
 ----QEGQGQTASHGELLTPVAGGP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
MEDLINE=87204263; PubMed=3033675;
Sikela J.M., Hahn W.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 315-469 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M16206; AAA39933.1; -. EMBL; M64266; AAA37364.1; -.
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 240-469 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J03057; AAA37366.1; -. X58995; CAA41741.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A29878; A29878.
PIR; S17656; S17656.
HSSP; Q63450; 1A06.
MGD; MGI:88258; Camk4.
                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                         430 KSSYCSEP 437
                                                   ----CVEP 358
                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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EMBL;
 325
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174 GIMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEET-ESKLFEKIK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 EGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTA--LHRDIYPS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 NCEYYFISPWWDEVSLNAKDLVKKLIVLDPKKRLITFQALQHPWVTGKAANFVHMD--T 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSK-MEQN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKSPAFRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGV 114
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      14 CSSVTASTENLVPDYWIDGSNRDPLGDFFEVESELGRGATSIVYRCKQKGTQKPYALKVL 73
                                                                                                                                                                                                                                                                                                                                                                                             9 CSSWKKQTTNIRKTF-----IFMEV---LGSGAFSEVFLVKQRLTGKLFALKCI 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tan J.L., Spudich J.A.; "Characterization and bacterial expression of the Dictyostelium myosin light chain kinase cDNA. Identification of an autoinhibitory domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 VSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETS 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 AQKKLQEFNARRKLKAAVKAVVASSRLGSASSSHTSIQENHKASSDPPSTQDAKDS 364
                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                         DB 1; Length 469;
                                                                                                                          ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
CALMODULIN-BINDING (POTENTIAL).
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00119; PROTEIN_KINASE_AT; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                       ; Score 697.5; DB 1; Length 4; Pred. No. 8.6e-37; 60; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spudich J.A., Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                     VLD -> CFGI (IN REF. 2).
N -> T (IN REF. 2).
CE1F98670822F975 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1992 (Rel. 22, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Myosin light chain kinase (EC 2.7.1.117) (MLCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                             PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 266:16044-16049(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91340753; PubMed=1651931;
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MEDLINE=90337997; PubMed=2380188;
                                                                                                                                                                                                                                                                   MM.
                                                                                                                                                                                                                                                                                                         27.8%; 42.7%; 1
                                                                                                      296
56
71
160
337
280
302
                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 42.7
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                              318
278
302
469 AA;
                                                                                      Calmodulin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                          ACT_SITE
DOMAIN
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                                                                                                                                                                                                                     CONFLICT
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                                                                                                                               NP_BIND
BINDING
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gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 HENGIVHRDLKPENLLYLTPEENSKIMITDFGLSK-MEONGIMSTACGTPGYVAPEVLAO 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 KPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDF 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 IKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRD--SSLENEIAVLKK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 265:13818-13824(1990).
                                       MYOSIN LIGHT CHAIN.
-!-CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin light-chain] phosphate.
-!- ENZYME REGULATION: POSSESSES AN AUTOINHIBITORY DOMAIN.
--- AUTOHUSPHORYALATION APPEARS TO INCREASE THE ENZYMATIC ACTIVITY.
DOES NOT HAVE A CALMODULIN-BINDING DOMAIN.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 295;
                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
"Dictyostelium myosin light chain kinase. Purification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY. 546CAEED8F6ECD0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                AUTOINHIBITORY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                         ATP (BY SIMILARITY). ATP (BY SIMILARITY).
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Pred. No. 7.6e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 6%; Scor.
50.2%; Pred. No. /...
                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN KINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 ICHLLEKDPNERYTCEKALSHPWIDGNTA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 IGKLLVVDVSKRLNATNALNHPWLKSNNS 270
                                                                                                                                                                                                                                                     HSSP, Q63450; 1A06.
DictyDb; DD01034; mlkA.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; I.
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                                                                                                                                                                                                                                                                                                          ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
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P13234;
01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                         33406 MW;
                                                                                                                                                                                                                       EMBL; M64176; AAB06337.1; -.
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                                                                                                                                                                                                                                  PIR; A40811; A40811.
PIR; A37125; A37125.
                                                                                                                   CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        295 AA;
                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00107;
           characterization
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SEQUENCE
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BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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KCC4_RAT
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-i. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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-:- ALTERNATIVE PRODUCTS: 2 isoforms; 1/calcium-calmodulin-dependent protein kinase type IV catalytic chain (shown here) and 2/calspermin; are produced by alternative splicing.
-:- TISSUE SPECIFICITY: Isoform 1 is expressed in brain and isoform 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE=96094352; PubMed=7493991;
Sun Z., Means R.L., LeMagueresse B., Means A.R.;
"Organization and analysis of the complete rat calmodulin-dependent
01-APR-1993 (Rel. 25, Last sequence update)
L-UN-2002 (Rel. 41, Last annotation update)
Calcium_calmodulin-dependent protein kinase type IV catalytic chain
(EC_2.7.1.123) (CAM kinase-GR) (CaMK IV) (Calspermin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A novel Ca2+/calmodulin-dependent protein kinase and a male germ cell-specific calmodulin-binding protein are derived from the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 306-474 FROM N.A. (ISOFORM 2), AND SEQUENCE OF 335-361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein kinase IV gene.";
J. Biol. Chem. 270:29507-29514 (1995).
-:- FUNCTION: CAM KINASE GR IS A NEURONAL-SPECIFIC PROTEIN KINASE,
ENRICHED IN CEREBELLAR GRANULE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley;
MEDLINE=89123272; PubMed=2914893;
Ono T., Slaughter G.R., Cook R.G., Means A.R.;
"Molecular cloning sequence and distribution of rat calspermin, a high affinity calmodulin-binding protein.";
J. Biol. Chem. 264:2081-2087(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Obmstede C.-A., Bland M.M., Merrill B.M., Sahyoun N.; Relationship of genes encoding Ca2+/calmodulin-dependent protein kinase Gr and calspermin: a gene within a gene."; Proc. Natl. Acad. Sci. U.S.A. 88:5784-5788(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohmstede C.-A., Jenson K.F., Sahyoun N.;
"Ca2+/calmodulin-dependent protein kinase enriched in cerebellar granule cells. Identification of a novel neuronal calmodulin-dependent protein kinase.";
J. Biol. Chem. 264:5866-5875(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISOFORMS 1 AND 2), AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Means A.R., Cruzalegui F., Lemagueresse B., Needleman D.S., Slaughter G.R., Ono T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is testis-specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 250-474 FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Sprague-Dawley; TISSUE-Brain;
MEDLINE-89174647; PubMed-2538431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell. Biol. 11:3960-3971(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AN)
MEDLINE-91288548; Pubmed-1648230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91304387; PubMed=1649385;
                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN.
--- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
--- SUBCELDULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL NUCLEI (BY SIMILARITY).
--- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mostalos G., Hanissian S.H., Jawahar S., Vara L., Kieff E., Chatila T.A.;

"A Ca2+/calmdulin-dependent protein kinase, CaM kinase-Gr, expressed after transformation of primary human B lymphocytes by Epstein-Barr virus (EBV) is induced by the EBV oncogene LMPI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                     MEDLINE-94375404; PubMed-8089075;
Kitani T., Okuno S., Fujisawa H.;
"cDNA cloning and expression of human calmodulin-dependent protein
     Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                            TISSUE-Cerebellum, and Thymus;
MEDLINE-94255566; PubMed-8194751;
Bland M.M., Monroe R.S., Ohmstede C.A.;
"The cDNA sequence and characterization of the
Ca2+/calmodulin-dependent protein kinase-Gr from human brain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94149862; PubMed=8107230;
                                                                                                                                                                                                                           kinase IV.";
J. Biochem. 115:637-640(1994).
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HSSP; Q63450; 1A06.
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60
75
        Eukaryota; Metazoa;
                            Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                                                                               SEQUENCE FROM N.A.
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52
75
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 YTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSK-MEQN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 GIMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEET-ESKLFEKIK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 VSLQIQKNFAKSKWRQAFNA-----BAVVHHMRKLHMNLHSPGVRP-----EV 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 CSSVTSSTENLVPDYWIDGSKRDPLSDFFEVESELGRGATSIVYRCKQKGTQKPYALKVL 73
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01-NOV-1997 (Rel. 35, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
calcium/calmodulin-dependent protein kinase type IV catalytic chain (EC 2.7.1.123) (CAM kinase-GR) (CAMK IV).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
CALMODULIN-BINDING (POTENTIAL).
POLY-GLU.
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PROSITE; PSOULOW; PROTEIN KINASE ST; 1.
PROSITE; PSOULOW; PROTEIN KINASE DOM; 1.
Transferase; Serine-threonine-protein kinase; ATP-binding; Calmodulin-binding; Testis; Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSING (IN ISOFORM 2).

I -> M (IN REF. 2 AND 4).

56F71AC5644DED23 CRC64;
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                                                                                                                                                                                                            InterPro; IPR000719; Buk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
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AAA40845.1; -. AAA40845.1; ALT_SEQ.
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                                                   EMBL; M64757; AAA40856.1; --
EMBL; M64777; AAA40857.1; --
EMBL; J046600; AAA41867.1; --
EMBL; J04446; AAA40990.1; --
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HSSP; Q63450; 1A06.
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474 AA;
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M63334; i
M74488; i
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Q16566;
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BINDING
ACT_SITE
DOMAIN
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Matches 149;
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                                                                            9
                                                                                                                    141
                                                                                                                                                                    200
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Subbaramaiah K., Greene V., Bartelt D.C.; "Structure of the cmkA gene encoding a CaMKII homolog in Emericella (Aspergillus) nidulans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kornstein L.B., Gaiso M.L., Hammell R.L., Bartelt D.C.;
Flooning and sequence determination of a cDNA encoding Aspergillus
nidulans calmodulin-dependent multifunctional protein kinase.";
Gene 113:75-82(1992).
                                                                                                                                                                                                                                                                        223 DMMSVGIITYILLCGFEPFYDERGDQFMFRRILNCEYYFISPWMDEVSLNAKDLVRKLIV
                                                                                                     FMEV---LGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRDSSLENEIAVLKKIKHENIV
                                                                                                                                                      82 TLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVH
                                                                                                                                                                                                         RDLKPENLLYLTPEENSKIMITDFGLSK-MEQNGIMSTACGTPGYVAPEVLAQKPYSKAV
                                                                                                                                                                                                                      DCWSIGVITYILLCGYPPFYEET-ESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLE
                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calcium/calmodulin-dependent protein kinase (EC 2.7.1.123) (CMPK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
--- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
--- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASSES.
CAMK SUBFAMILY:
                                                                            12;
                                                                                                                                                                                                                                                                                                                                     283 LDPKKRLTTFQALQHPWVTGKAANFVHMD---TAQKKLQEFNARRKLKAAVKA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
BY SIMILARITY.
CALMODULIN-BINDING (POTENTIAL).
EFEE51E5612326DC CRC64;
                                                    Length 473;
                                                                                                                                                                                                                                                                                                             260 KDPNERYTCEKALSHPWIDGNTA - - LHRDIYPSVSLQIQKNFAKSKWRQAFNA
                                                                            87; Indels
                                                                ; Pred. No. 6.1e-36; 53; Mismatches 87
                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Emericella nidulans (Aspergillus nidulans)
                                                                                                                                                                                                                                                                                                                                                                                                      414
                                                  27.2%; Score 684;
48.1%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF054580; AAD22581.1; -.
HSSP; 063450; 1A06.
Interpro; IPR000719; Euk_pkinase.
Interpro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                         51925 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M74120; AAB97502.1; -.
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
164
322
473 AA;
                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5072;
                                                                          Matches 141;
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Q00771;
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ACT_SITE
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                                                    Query Match
                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=20541713; PubMed=11087665;
Brede G., Solhelm J., Troen G., Prydz H.;
"Characterization of PSKH1, a novel human protein serine kinase with centrosonal, golgi, and nuclear localization.";
Genomics 70:82-92(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
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MEDILINE-87092414; PubMed-2948189;
Hanks S.K.;
"Homology probing: identification of cDNA clones encoding members of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 RKTFIFMEVLGSGAFSEVFLVKQR--LTGKLFALKCIKKSPAFRDSSLENEIAVLKKIKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 KSLYRFGRTLGAGTYG---IVREADCSSGKVAVKIILKRNVRGNERMVYDELDLLQKLNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 ENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQN--GIMSTACGTPGYVAPEVLAQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 YSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 HMRKLHMNLHSPGVRPEVENRPP--ETQASETSRPSSPEITITEAPVL--DHSVALPALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 RIEALKMQ-----EEDEEDIPSAVDVQASEASDKSG----LSPFPALSTENSNTHPAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                           Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FPSH_HUMAN STANDARD; PRT; 424 AA.
P11801; Q9NY19;
01-OCT-1989 (Rel. 12, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase H1 (EC 2.7.1.37) (PSK-H1).
                                                                                                                                                                                                                                                                                                                                          CALMODULIN-BINDING (BY S. 1E8D58A1C0B2F18C CRC64)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78; Mismatches 126;
                                                                                                                                                                                                                                                        ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
Pfam; PF00069; pkinase; 1.

Prodom; PD000001; Euk_pkinase; 1.

SMART: SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_LOM; 1.

PROSITE; PS00101; PROTEIN_KINASE_LOM; 1.

PROSITE; PS00101; PROTEIN_KINASE_LOM; 1.

Phosphorylation; ATP_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                          25.9%; Score 651; DB 1
38.3%; Pred. No. 6e-34;
                                                                                                                                                                                                                                 PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 QLPCQHGRRPTAPGG---RSLNCLVNGSL 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 ----GNGE----SGGTKKRSLSKIARGAI 383
                                                                                                                                                                                                                                                                                                                                                                       46889 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                 278
                                                                                                                                                                                                                                                                                                                                          291
414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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(CaMK-I)
                                                                                                                                                                                                                  pombe.
                       RESULT 9
                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLLYLTPEENSKIMITDFGLSKMEQNG---IMSTACGTPGYVAPEVLAQKPYSKAVDCWS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 VLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRDSSLENEIAVLKKIKHENIVTLEDIY 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AASSSMKNLHRSI
                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (POTENTIAL)
PHOSPHORYLATION (AUTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 424;
                                                                                                                                                                                                                                                                            PERMIT PROUGS) PAINASE.
PERMIT PROUGS) PAINASE.
PERMIT SMO0220; STRC; 1.
SMART; SMO0220; STRC; 1.
PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE; PSO0108; PROTEIN_KINASE_ATP; 1.
PROSITE; PSS00119; PROTEIN_KINASE_DOM; 1.
PROSING*/LIREONING-PROTEIN KINASE_POM; 1.
PROSPHOFYLATION; GOLGI stack; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           B357757DDC12388D CRC64;
                                                                                                                                                                                                                                                                                                                                                                  PROTEIN KÎNASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.8e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              25.6%; Score 643.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RMTALQALRHPWV------VSM----
                                                                                                                                                                                                                                               Interpro; IPR000719; Euk_pkinase.
Interpro; IPR002290; Ser_thr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 -SQNLLKRASSRCQSTKSAQSTRSS 395
                                                                                                                                                                                          EMBL; AJ272212; CAB91984.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                           48035 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.0%;
                                                                                                                                                                                                    EMBL; M14504; AAA36519.1;
PIR; B26368; B26368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 40.0 Matches 130; Conservative
                                                                                                                                                                                                                      HSSP; Q63450; 1A06.
Genew; HGNC:9529; PSKH1.
MIM; 177015; -.
                                                                                                                                                                                                                                                                                                                                                                                                                           424 AA;
                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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BINDING
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REC STRANS-919.

REC STRANS-919.

REC STRANS-919.

RA MEDLINE-21848401; Pubbed=11859360;

RA God V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Squuros J., Peat N., Hayles J., Baker S., Basham D., Bowaman S., A Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Felewell T., Fraser A., Collins M., Connor R., Cronin A., Davis P., Felewell T., Fraser A., Gontor S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holres S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., R. Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J., RA Gontes L., Jones M., Cather S., McDonald S., McLean J., RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., R. Rutherford K., Taylor R., Saudres R., Squares S., Stevens K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Mitchead S., RA Taylor K., Taylor R., Taylor R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabler C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Rablert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Raga R.R., Cuzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Sanchez M., del Rey F., Benito J., Moreno S., Armstrong J., Porsburg S.L., R. Spakovski G.V., Ussery D., Barrell B.G., Nurse P., Nature 415:871-880(2002).

R. Shapkovski G.V., Ussery D., Barrell B.G., Nurse P., R. The genome sequence of Schizosaccharomyces pombe.";

R. The genome sequence of Schizosaccharomyces pombe.";

R. The genome sequence of Schizosaccharomyces pombe.";

R. Stakler J. Staklers LOCATIVITY: ATP + Protein = ADP + O-phosphorotein.

C. Terralmity T. Stakler S. The SER/THR FAMILY OF PROFEIN KINSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION, AND MUTAGENESIS OF THR-192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of a calmodulin kinase I homologue from Schizosaccharomyces
| CCCI_SCHPO | STANDARD; | PRT; | 335 AA. |
| Q9P712; | 074235; |
| 16-0CT-2001 (Rel. 40, Last sequence update) |
| 16-0CT-2001 (Rel. 40, Last sequence update) |
| 15-JUN-2002 (Rel. 41, Last annotation update) |
| Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123) |
                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20085094; PubMed=10617667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 275:685-690(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF073893; AAC26005.1; -. EMBL; AL157993; CAB76233.1; -. HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                       CMK1 OR SPAC25D11.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAMK SUBFAMILY
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TISSUE-Fetal brain;
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                                                                                                                                                                                                                                                                                                                          261
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                                                                                                                                                                                                                                                 144
                                                                                                                                                                                                                                                           Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. VII.
The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                           12; Gaps
                                                                                                                                                                                                                       28 VLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIAVLKKI--KHENIVTLE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase DCAMKL1 (EC 2.7.1.-) (Doublecortin-
Like and CAM kinase-like 1).
DCAMKL1 OR KIAA0369.
                                                                  g; Phosphorylation.
291 PROTEIN KINASE.
293 ATP (BY SIMILARITY).
334 CALMODULIN-BINDING (POTENTIAL).
154 BY SIMILARITY.
192 PHOSPHORYLATION (AUTO-).
192 T->D: 15-FOLD INCREASE IN ACTIVITY.
295 KR -> NG (IN REF. 1).
295 KR -> NG (IN REF. 1).
                                                                                                                                                                                                                                                                                               DIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDL
                                                                                                                                                                                                                                                                                     145 KPENLLYLTPEENSKIMITDFGLSKMEQNG---IMSTACGTPGYVAPEVLAQKPYSKAVD
                                                                                                                                                                                                                                                                                                                        202 CWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                         Length 335;
Pfam; PF00069; pkinase; 1.
SMART; SM00200; Euk_pkinase; 1.
SMART; SM00210; ZTKc; 1.
PROSITE; PS00107; PROTEIN, KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS010108; PROTEIN_KINASE_ST; 1.
ATP-binding; Serine-Chreonine-protein kinase; Transferase; Calmodulin-binding; Phosphorylation.
                                                                                                                                                                       25.1%; Score 630; DB 1; Length 33:
43.6%; Pred. No. 9.7e-33;
tive 56; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 740 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A. (ISOFORMS AS AND AL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e for large proteins in vitro."; Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97349984; PubMed-9205841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM AS).
                                                                                  45
110 334
54 195
2 192
192
295
295
38163 MW;
                                                                                                                                                                                Best Local Similarity 43.68 Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                         192
115
294
335 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DCK1_HUMAN
                                                                                                     ACT_SITE
MOD_RES
                                                                                                                                    CONFLICT
                                                                                                                                                      SEQUENCE
                                                                                                                                                                         Query Match
                                                                                     UP_BIND
                                                                                                                          MUTAGEN
                                                                             DOMAIN
                                                                                               DOMAIN
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CONTRACTOR TO THE STATE OF A LEADY A SHORT (BA) AND LONG (AL) (SHOWN HERE). TYPE B SHORT (BS) AND LONG (AL); ARE PRODUCED BY ALTERNATIVE SPLICING. TYPE A AND TYPE B ISOFORMS DIFFER RESPECTIVELY BY THE PRESENCE OF THE DOUBLECORTIN DOMAIN. AN ALTERNATIVE SPLICING OCCURRING IN 3' OF THE MRNA PRODUCES THE LONG INSTEAD OF THE SHORT ISOFORMS.

1 TISSUE SPECIFICITY: IN FETAL TISSUES, HIGHLY EXPRESSED IN BRAIN, DETECTABLE IN LUNG AND LIVER, BUT NOT IN KIDNEY. IN ADULT TISSUES, EXPRESSED UBIQUITOUSLY IN THE BRAIN, DETECTABLE IN THE HEART, INTESTINE AND COLON. THE TYPE A ISOFORMS SEEM TO BE EXPRESSED ABUNDANTLY IN FETAL BRAIN WHEREAS TYPE B ISOFORMS ARE EXPRESSED ABUNDANTLY IN SETAL BRAIN WHEREAS TYPE B ISOFORMS ARE EXPRESSED ABUNDANTLY IN SETAL BRAIN WHEREAS TYPE B ISOFORMS ARE EXPRESSED ABUNDANTLY IN COMMESSED.

1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

2 CAME SUBBRAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Blainformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -I- FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-
SIGNALING PATHWAY CONTROLING NEURONAL MIGRATION IN THE DEVELOPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; TYPE A SHORT (AS) AND
MEDLINE-99156863; PubMed-10036192; Sossey-Alaoul K., Srivastava A.K.; "DCAWKL1, a brain-specific transmembrane protein on 13q12.3 that is similar to doublecortin (DCX).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY.
MEDLINE-99162404; PubMed-10051403;
Matsumoto N., Pilz D.T., Ledbetter D.H.;
"Genomic structure, chromosomal mapping, and expression pattern of human DCAMKL1 (KIAA0369), a homologue of DCX (KLIS).";
Genomics 56:179-183(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        !ransferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                Omori Y., Suzuki M., Ozaki K., Harada Y., Nakamura Y., Takahashi E.-I., Fujiwara T.; Farada T.; Fujiwara T.; Expression and chromosomal localization of KIAA0369, a putative kinase structurally related to Doublecortin."; J. Hum. Genet. 43:169-177(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SER/PRO-RICH.
PROTEIN KINASE.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS AS; AL; BS AND BL). MEDLINE=98419166; PubMed=9747029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurogenesis; Alternative splicing.

DOMAIN 57 143 DOUBLECORTIN 1.

DOMAIN 186 269 DOUBLECORTIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probon; PD000001; Euk_pkinase; 1.
SMART; SM0537; DCX; 2.
SMART; SM0220; S_TKC; 1.
SMO51E; PS50309; DC; 2.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM: 604742; ...
InterPro; IPR003533; DCX.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Sex_thr_pkinase.
Pfan; PP00069; pkinase; 1.
Pfan; PF03607; DCX; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB002367; BAA20824.1; -.
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                                                                                                                                                                    Genomics 56:121-126(1999)
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DOMAIN
NP_BIND
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DOUBLECORTIN 1.
DOUBLECORTIN 2.
SER/PRO-RICH.
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                                                                                                                                                                                                                                                                                                                                    PROTEIN_KINASE_ATP; 1.
PROTEIN_KINASE_DOM; 1.
PROTEIN_KINASE_ST; 1.
                                                                                                         EMBL; AF155819; AAF26673.1; -. HSSP; Q63450; 1A06. MGD; MG1:1330861; Dcamkll. InterPro; IPR003533; DCX. InterPro; IPR0003533; DCX. InterPro; IPR0002199; Suk_pkinase. Pfam; PF00066; pkinase; 1. Pfam; PF00669; DCX; 2.
                                                                                                                                                                                                                                                               ProDom; PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84153 MW;
                                                                                                                                                                                                                                                                                 SMART; SM00537; DCX; 2.
SMART; SM00220; S_TKC; 1.
PROSITE; PS50309; DC; 2.
PROSITE; PS00107; PROTEIN_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 36.7
Matches 137; Conservative
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269
358
663
420
435
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298
406
412
435
527
756 AA;
                                                                                                                                                                                                                                                                                                                                                             PS50011;
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SEQUENCE
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DOMAIN
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NP_BIND
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KCCB_HUMAN
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                                                                                                                                                                                                                                                               8
                                                                                                               ITALDKERQVFRRRRNQDVRSRYKAOPAPPELNSESEDYSP
                                                                                                                              SSSETVRSPNSPF -> LDHGFTIKRSGSLDYYQQPGMYWI
RPPLLIRRGRFSDEDATRM (IN ISOFORM AS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Neurosci. Res. 58:567-575(1999).

-!- FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-
SIGNALING PATHWAY CONTROLING NEURONAL MIGRATION IN THE DEVELOPING
BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS
SYSTEM (By similarity).

-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                        : | ||||:|| ||:||| || |||:||| 456 DVPTELYLVMELVKGGDLFDAITSTNKYTERDASGMLYNLASAIKYLHSLNIVHRDIKPE 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 RYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNF-------AKSKWR 305
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                                                                                                                                                                                                                                                                                                                                                                            ESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPE 147
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                  LGSGAFSEVFLVKQRLTGKLFALKCIKKSPA-FRDSSLENEIAVLKKIKHENIVTLEDIY 87
                                     POLY-ARG.
MISSING (IN ISOFORM BS AND ISOFORM BL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
18-JUN-2002 (Rel. 41, Last annotation update)
19-JUN-2002 (Rel. 41, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NILYLTPEENSK-IMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPYSKAVDCWSIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VITYILLCGYPPF - YEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:: : | | | | | :: : | | | | 635 RFSAVQVLEHPWYNDDGLPENEHQLSVAGKIKKHFNTGPKPNSTAAGVSVIATTALDKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                          PASTSS -> MLELIE (IN ISOFORM BS AND ISOFORM BL).
                                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burgess H.A., Martinez S., Reiner O.;
"KIAA0369, doublecortin-like kinase, is expressed during brain
development.";
                                                                                                                                                                                                                          DB 1; Length 740;
                                                                                                                                                                                                                        ; Score 612; DB 1; Length 740; Pred. No. 3.4e-31; 69; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 QAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQA-SETSRPSSPE 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISOFORM BS).
D7B6D855099A315C CRC64;
 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 2 DOUBLECORTIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  756 AA
                     SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
MEDLINE=20004649; PubMed=10533048;
                                                                                                                                                                                     82223 MW;
                                                                                                                                                                                                                          24.4%;
39.1%;
                                                                                                                                                                                                                                                             136; Conservative
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 419
511
701
307
313
                                                                                                             740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                     740 AA;
                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAMK SUBFAMILY
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419
511
698
                                                          1
308
                                                                                                             687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCK1_MOUSE
BINDING
ACT_SITE
DOMAIN
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                        Query Match
                                                      VARSPLIC
                                                                          VARSPLIC
                                                                                                             VARSPLIC
                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                29
                                                                                                                                                                                                                                                                                                                                                                                                                                                     148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447 HMIQNEVSILRRVKHPNIVLLIEEMDVPTELYLVMELVKGGDLFDAITSTSKYTERDASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WKKQTT-----NIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPA-FRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 VIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSK-IMITDFGLSKMEQNGIMSTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 SPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -------AKSKWRQAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPET

        RCCB_HUMAN
        STANDARD;
        PRT;
        664 AA.

        Q13554;
        O95437;
        O95599;
        Q9UGH7;
        Q9UGH9;
        Q9UNXO;

        Q9UNXO;
        Q9Y5N4;
        Q9Y6F4;
        Created)
        C1-NOY-1997 (Rel. 35, Created)
        Created)
        L6-CCT-2001 (Rel. 40, Last sequence update)

        15-JUN-2002 (Rel. 41, Last annotation update)
        L6-JUN-2002 (Rel. 41, Last annotation update)
        L6-JUN-2002 (Rel. 41, Last annotation update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.1%; Score 606; DB 1; Length 75.36.7%; Pred. No. 8.2e-31;
ive 76; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
3DIDBF18C23129F2 CRC64;
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us-09-960-643-2.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS: 7 ISOFORMS; 0/BETA, 1/BETA1/BETA'E, 2/BETA2, 3 (SHOWN HERE), 4/BETA4/BETAE, 6/BETA6 AND 7/BETA7; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                    the beta subunit
II with different
2.7.1.123) (Caw-kinase Type II beta chain (EC (CaMK-II beta subunit) (Cam kinase II beta subunit) CAWK2B OR CAMKB OR CAMKB OR CAMKB OR CAMKB OR CAMKB OR CAMKB OR CAWR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-Insullinoma, WEDLINE-20277365; PubMed-10819240; MEDLINE-20277365; PubMed-10819240; Rochlitz H., Volgt A., Lankat-Buttgereit B., Goke B., Heimberg H., Nauck M.A., Schlemann U., Schatz H., Pfeiffer A.F.; "Cloning and quantitative determination of the human ca2+/calmodulin-dependent protein kinase II (CaMK II) isoforms in
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                            Li G.Y., Cooper N.G.F.; "Mocaular cloning and sequencing of human calcium/calmodulin appearant protein Kinase II beta subunit."; Submitted (DEC-1998) to the EMBL/GenBank/PDBJ databases.
                                                                                                                                                                                                                                                                                                                             TISSUE-Skeletal muscle;
Leddy J.J., Salih M., Tuana B.S.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                  Wang P., Wu Y., Zhou T.H., Sun Y., Pei G., "Identification of alternative splicing variants of of human Ca(2+)/calmodulin-dependent protein kinase
                                                                                                                                                     [1]
SEQUENCE FROM N.A. (ISOFORMS 0; 1; 4; 6 AND 7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 0 AND 4).
                                                                                                                                                                                                  MEDLINE-20317016; PubMed-10858498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AF081572, AAD42036.1; --
EMBL, AF083419, AAD42038.1; --
EMBL, AF081924; AAD42037.1; --
EMBL, AF140350; AAD42070.1; --
EMBL, AF140346; AAC99802.1; --
EMBL, AF114772; AAD03744.1; --
EMBL, AF112471; AAD03743.1; --
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diabetologia 43:465-473(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF078803; AAD42035.1; -.
                                                                                                                                                                                                                                                                                FEBS Lett. 475:107-110(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human beta cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                rISSUE-Brain;
                                                                                                                                                                                     IISSUE-Brain
                                                                                                                                                                                                                                                                     activities."
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12;
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MISSING (IN ISOFORM 1, ISOFORM 2 AND ISOPORM 4).
MISSING (IN ISOFORM 7).
MISSING (IN ISOFORM 6).
MISSING (IN ISOFORM 1).
MISSING (IN ISOFORM 1).
MISSING (IN ISOFORM 1).
MISSING (IN ISOFORM 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | : | : | : | : | : | 367 TMLATRNFSVGRQTTAPATMSTAASGTTMGLVEQAKSL-LNKKADGVKPQTNSTKNSAAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNF-AKSKWRQAF-- 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 TQASETSRPSS--PEITITEAPV------LDHSVALP----ALTQLPCQHGR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 IKHENIVILEDIYESTTHYYLVMQLVSGELFDRILERGVYTEKDASLVIQQVLSAVKYL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 INIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI--KKSPAFRDSSLENEIAVLKK 74
                                                                                                                                                                                                                                                                                                                                                  FROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY).

CAMADOLIN-BINDING.

V -> A (IN ISOFORM 1, ISOFORM 2 AND ISOFORM 4).
                                                                                                                                                                                                                                                                                              Transferaes: Serine/threonine-protein kinase; Calmodulin-binding; Phosphorylation; ATP-binding; Neurone; Alternative splicing. DOMAIN PLIND 20 28 ATP (BY SIMILARITY). BINDING 43 43 ATP (BY SIMILARITY). ACT_SITE 136 BY SIMILARITY. DOMAIN 291 301 CALMODULIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 NLINQMLTINPAKRITAHEALKHPWVCQRSTVASMMHRQETVECLKKFNARRKLKGAILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 HENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMST---ACGTPGYVAPEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 AQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 TSPKGTLPPAALEPQTTVIHNPVDGIKESSDSANTTIEDEDAKAPRVPDILSSVRRGSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380 R----PTAPGGRSLNCLVNGSLHISSSL-----VPMHQGSLAAGPCGCCSSCL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSRGAPACPSPAPFSPLPAPSPRISDILNSVRRGSGTPEAEGPLSAGPPPCLSPAL 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.0%; Score 603.5; DB 1; Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9E8C82918D986814 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L -> V (IN REF. 3)
K -> N (IN REF. 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1e-30;
                                                                                                                                                                                                                 ProDom; PD000001; EUK_pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                       EMBL, US0358; AAB16863.1; -.
Genew, HGNC:1461; CAMK2B.
INTERPRO; IPR000719; EUK_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
AJ252237; CAB65120.1; -. AJ252237; CAB65121.1; -. AJ25238; CAB65121.1; -. GAB65122.1; -. GAB6512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72726 MW;
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393
531
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68
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533
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354
354
379
410
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Matches 158;
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VARSPLIC
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                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252
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RESULT 13 DCK1_RAT

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CGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPF--YEETESKLFEKIKEGYYE 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:1460; CAMK2A.
MIM; 114078; -.
                                                                                                                                                                        ETQA-SETSRPSSPE 352
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                               (CaMK-II alpha subunit).
                                                                                                                                                                                                 ELNSESEDYSPSSSE 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G.Y., Cooper N.G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR002290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAMK SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  063450;
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                                                                                                                    NF----
                                                                                                                                                                                                                                                                  KCCA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                          Hevroni D., Rattner A., Bundman M., Lederfein D., Gabarah A.,
Mangelus M., Silverman M.A., Kedar H., Naor C., Kornuc M., Hanoch T.,
Seger K., Theill L.E., Nedivi E., Richter-Levin G., Citri Y.;
"Hippocampal plasticity involves extensive gene induction and multiple
cellular mechanisms.";
                                                                                                                                                                                                                                                                                           SIGNATION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-SIGNALING PATHWAY CONTROLING NEURONAL MIGRATION IN THE DEVELOPING BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGMLYNLASAIKYLHSLNIVHRDIKPENLLVYEHQDGSKSLKLGDFGLATI-VDGPLYTV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSK-IMITDFGLSKMEQNGIMSTA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ||: :: || || || || GPGEESDEGFQIPAT-ITERYKVGRTIGDGNFAVVKECIERSTAREYALKIIKKSKCRG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEHMIQNEVSILRRVKHPNIVLLIEEMDVPTELYLVMELVKGGDLFDAITSTSKYTERDA 181
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPA-F 60
               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Serine/threonine-protein kinase DCAMKL1 (EC 2.7.1.-) (Doublecortin-like and CAM kinase-like 1) (Calcium/calmodulin-dependent protein kinase type I-like CPG16).
                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.0%; Score 602.5; DB 1; Length 433; 37.1%; Pred. No. 7e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000719; Buk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Probom; PD000001; Buk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00108; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
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OCESE06E152A557D CRC64;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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 433 AA
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                                                                                                                                                                                                            MEDLINE=98364306; PubMed=9699150;
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HSSP; Q63450; 1A06.
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                                                                                                                    Rattus norvegicus (Rat).
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340
394
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112
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83
391
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112
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433 AA;
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Matches 139; Conserv
                                                                                                                                                                                                                                                                                                                                                                           CAMK SUBFAMILY
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                  STRAIN=Wistar;
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SEQUENCE
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NP_BIND
BINDING
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-i- CATALTICA CATULITY: ATP + protein = ADP + 0-phosphoprotein.
-i- ENZYME REGULATION: Autophosphorylation of Thr-286 allows the kinase to switch from a calmodulin-dependent to a calmodulin--:- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are produced by alternative splicing.
-:- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. and gene analysis."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. independent state (By similarity). A. 478 SMART: SMO0220: S. TKC; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP;
PROSITE: PS50011; PROTEIN_KINASE_DOM; Ser_thr_pkinase. PRT; Pfam; PF00069; pkinase; 1. ProDom; PD000001; Euk_pkinase; 1. InterPro; IPR000719; Euk_pkinase. EMBL; AF145710; AAD30558.1; -. AF145711; AAD30559.1; -.

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                                                                                                                                                                                                                                                                                                                     HENGIVHRÖLKPENLLYLTPEENSKIMITDFGLS---KMEQNGIMSTACGTPGYVAPEVL 191
                                                                                                                                                                                                                                                                                                                                    ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                           192 AQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAK 251
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                               75 IKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                    7 TRFTEEYQLFEELGKGAFSVVRRCVKVLAGQEYAAKIINTKKLSARDHQKLEREARICRL 66
                                                                                                                                                                                                           17 THIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI--KKSPAFRDSSLENEIAVLKK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calcium/calmodulin-dependent protein kinase type II alpha chain (EC 2.7.1.123) (CaM-kinase II alpha chain) (CaM kinase II alpha subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-87289722; PubMed-3475713;
Lin C.R., Kapiloff M.S., Durgerian S., Tatemoto K., Russo A.F.,
Lanson P., Schulman H., Rosenfeld M.G.;
"Molecular cloning of a brain-specific calcium/calmodulin-dependent
protein kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 132-327 FROM N.A.
MEDLINE-87263392; PubMed-3037704;
Hanley R.M., Means A.R., Ono T., Kemp B.E., Burgin K.E., Waxham N.,
                                                                                                                                                                                                                                                                                                                                                                                             Punctional analysis of a complementary DNA for the 50-kilodalton subunit of calmodulin kinase II.";
Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
                                                                                                                                                                                10;
                                                                                                            -> KKRKSSSSVQLM (IN ISOFORM B).
10800A85CAD724BB CRC64;
                                                                                                                                                     Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357
                                                                                                                                                   24.0%; Score 602; DB 1; Length 470
39.1%; Pred. No. 8.4e-31;
.ive 58; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 AAVVHHM---RKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 IMLATRNFSGGKSGGNKKSDGVKESSESTNTTIEDEDTKVRKQEIIKVTE
        Alternative splicing. PROTEIN KINASE.
                                                                                               CALMODULIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84:5962-5966(1987)
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             hosphorylation; ATP-binding;
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                                                                                                                      54029 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 237:293-297(1987).
                                                                                                                                                                  Best_Local Similarity 39.13
Matches 137; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                           271
27
42
135
286
300
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286
290
328
478 AA;
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BINDING
ACT_SITE
MOD_RES
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SEQUENCE
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VARSPLIC
SEQUENCE
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                           DOMAIN
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R EMBL; M19960; AAA41855.1; -.

R EMBL; M31235; AAA40841.1; -.

R PIR; A31235; A31235.

R PIR; A30355; A30355.

R InterPro; IPR00219; Euk_pkinase.

R InterPro; IPR00290; Ser_thr_pkinase.

R Probom; PD000001; Buk_pkinase; 1.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS0011; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS0011; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKHPNIVRLHDSISEEGHHYLIFDLVTGGELFEDIVAREYYSEADASHCIQQILEAVLHC 126
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                                                                                                                                                                                                                            MEDLINE-88320438; PubMed-2842767;
MIPLE G. CZEATHA A.J. GOTELICK F., Nairn A.C., Greengard P.;
"Ca2+/Calmodulin-dependent protein kinase II: identification of threonine-286 as the autophosphorylation site in the alpha subunit associated with the generation of Ca2+-independent activity.";
Proc. Natl. Acad. Sci. U.S.A. 85:637-644(1988).
--- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
--- CATALITIC ACTIVITY: ATP + protech. A DP + O-phosphoprotein.
--- CATALITIC ACTIVITY: Attophosphorylation of Thr-286 allows the kinase to switch from a calmodulin-dependent to a calmodulin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 independent state.
-1- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
                             Sunyer T., Sahyoun N.; "Sequence analysis and DNA-protein interactions within the 5' flanking region of the Ca2+/calmodulin-dependent protein kinase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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G -> A (IN REF. 2).
306F416CCE9B5F62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (AUTO-).
                                                                                                                                                                                                 SEQUENCE OF 282-299, AND PHOSPHORYLATION OF THR-286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 87:278-282(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE
MEDLINE=90115857; PubMed=2153289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59;
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290
301
478 AA;
                                                                                                                 alpha-subunit gene.
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  g
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Qy
Db
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0y 0b

311 AAVVHHW---RKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITE 357 : | | : | | : | | : | | 306 TMLATRNFSGGKSGGNKKNDGVKESSESTNTTIEDEDTKVRKQEIIKVTE 355

Search completed: March 14, 2003, 14:08:58 Job time: 17 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 14, 2003, 14:07:31 ; Search time 18 Seconds
 (without alignments)
 2542.221 Million cell updates/sec

US-09-960-643-2 2513 1 MGRREEDDCSSWKKQTTNIR.....VKASGSSHCRAGQTGVCLIM 476 Title: Perfect score: Sequence:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR 73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Ca2+/calmodulin-de Ca2+/calmodulin-de Ca2+/calmodulin-de protein K07A9.2 [i calmodulin-binding calmodulin-binding Ca2+/calmodulin-de Ca2+/calmodulin-de	2+/calmodulin 0sin-light-ch 2+/calmodulin 2+/calmodulin 1modulin kina 2+/calmodulin pothetical pr 2+/calmodulin	Caz+/calmodulin-de
SUMMARIES			
SUMP.	S50193 S57347 T37321 B88640 I56542 T30814 S17656 TVRTC4	152637 A40817 50817 50817 50818	0 7 0 7
DB			4
Length	3374 3370 310 348 370 374 374 374	502 4 4 7 3 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2	*
% Query Match		2.7.7.4.4.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.	'n
Score	1155.5 1152.5 1004 880 736 703 697.5 692.5	6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.00
Result No.	H C W 4 N O C & O	0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1

Ca2+/calmodulin-de	calcium-dependent	probable serine-th	Ca2+/calmodulin-de	calcium-dependent	protein kinase RAD	calcium-dependent	calcium-dependent	probable calcium d	probable calcium-d	hypothetical prote	protein-serine kin	calcium-dependent	calcium-dependent	calcium-dependent	calcium-stimulated
A40896	T05476	T38226	A31908	S71776	A39616	A49082	T08873	F85059	H84810	T33690	138138	A43713	S46284	T02139	S54788
7	7	7	Н		~	-	7	7	7	7	7	Н	Н	7	7
446	554	504	527	490	821	610	490	520	583	443	319	208	495	553	591
23.0	22.8	22.7	22.5	22.3	22.2	22.1	22.0	21.7	21.7	21.6	21.6	21.6	21.6	21.5	21.5
577.5	573	569.5	566.5	559.5	558	556.5	553	546.5	544.5	544	543.5	543.5	543	541.5	541.5
57															

ALIGNMENTS

	RESULT 1
	Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - rat
_	C; Species: Rattus norvegious (Norway rat)
	C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
	R;Cho, F.S.; Phillips, K.S.; Bogucki, B.; Weaver, T.E.
	A; Reference number: S50193; MUID:95035115; PMID:7948038
	A;Accession: S50193
_	A; reaus: pretiminary A; Molecule type: mRNA
	A; Residues: 1-374 <cho></cho>
	A:Coss-references: EMBL:L26288; NID:949613; PIDN:AAA66944.1; PID:9439614
_	7. Biol. Chem. 268, 26512-26521, 1993
	A/Title: Calcium/calmodulin dependent protein kinase I. cDNA cloning and identificat
	A:Reference number: A49682; MUID:940/5341; PMID:8253/80
	ACACCESTOUR AFFORZ ACACCE
_	A:MOLECULE TOTALITION A MOLECULE TO A MOLECULE TO A MRNA
	A; Residues: 1-111, 'G', 113-117, 'R', 119-308, 'R', 310-322, 'HQPG', 327, 'T', 329, 'TDS' <pic></pic>
	A;Cross-references: GB:L24907; NID:g406112; PIDN:AAA19670.1; PID:g406113
_	R; Mochizuki, H.; Ito, T.; Hidaka, H.
	J. Biol. Chem. 268, 9143-9147, 1993
) Militie: Fullitacijul anu vinatacielizaciju ol cazifoziju Alberpane number: A46038. MITD-93232082. DMID-8386178
	A; Accession: A46038
	A;Status: preliminary
	A Molecule type: protein
_	A. Restaudes: 12 -00, 1 AOC. A. Restaudes: 12 -00, 1 AOC.
	A; Note: sequence extracted from NCBI backbone (NCBIP:129927)
	C;Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology
_	C; Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotra
	F:3E-2/6/Domin: Procein Kinase homology <pre> F:3E-2/6/Domin: Procein kinase homology <pre> F:36-34/poxion: protein binase publishinging metif</pre></pre>
	F:293-299/Redion: autoinhibitory
	F;302-314/Region: calmodulin binding
	F;177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred
	Query Match 46.0%; Score 1155.5; DB 1; Length 374;
	Best Local Similarity 69,68; Pred, No. 6.9e-44; Matches 272: Concervative A3: Mismatches 41: Indole 3: Gane 3:
	272
	OY 12 WKKQTTNIRKTFIFWEVLGSGAFSEVFLVKQRLFGKLFALKCI-KKSPAFRDSSLENEIA 70
	Db 10 W-KQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIA 68

71 VLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSA 130

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qa å		
g G	VALUDENGLYBROUNFERGLEITEREBNOSIMITERGLESMEEGNG IMSTRAGIFGIYARE :	
Qy Dp	190 VLAQKRYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISES 249 	Qy 430 KSSXCSEP 437 Db 355CVEP 358
Qy	250 AKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFN 309 	
yo 4	310 AAAVVHHRKLHMNLHSPG 328 328	Ca2+/Caimodulin-dependent process (EC 2.7.1.123) 1 Caessols elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000 C.Accession: 717721
RESULT S57347		R;Eto, K.; Takahashi, N.; Kimura, Y.; Masuho, Y.; Arai, K.; Muramatsu, M.; Tokumitsu, J. Blol. Chem. '74, 22556-22552, 1999 A;Title: Ca2+/Calmodulin-dependent protein kinase cascade in Caenorhabditis elegans. A;Reference number: 221686; MUID:99357789; PMID:10428833
Caz+ N; Al	123) 1 - numan	A;Accession: 13.34. A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
C; Da	C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: S57347 R;Haribabu, B.; Hook, S.S.; Selbert, M.A.; Goldstein, E.G.; Tomhave, E.D.; Edelman, A.M.	A; Residues: 1-348 <eto> A; Cross-references: EMBL:AB021864; NID:95672677; PIDN:BAA82674.1; PID:95672678 A; Experimental source: strain Bristol N2; embryonic stage</eto>
A;Ti	LANDO V. 14, 2013 2000, 1333 A,Title: Human calcium-calmodulin dependent protein kinase I: cDNA cloning, domain struc A,Reference number: S57347; MUID:95369239; PMID:7641687	A; Note: cmx-1 C; Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology C; Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotran
A; Ac A; St A; Mo A; Re		Query Match 40.0%; Score 1004; DB 2; Length 348; Best Local Similarity 57.3%; Pred. No. 2.5e-37; Matches 185; Conservative 67; Mismatches 69; Indels 2; Gaps 2;
A; Ge A; Ge A; Cr	2	QY 19 IRKTFIFMEVLGSGAFSEVFLVKQRL-TGKLFALKCI-KKSPAFRDSSLENEIAVLKKIK 76 :: : : : :: :: :: :: :: :: :: Db 18 IREKYDFRDVLGTGAFSKVFLAESKSDAGQMYAVKCIDKKALKGKEESLENEIKVLRKLR 77
C; St C; Ke F; 18	Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfe 18-276/Domain: protein kinase homology <kir). 26-34="" atp-binding="" kinase="" motif<="" protein="" region:="" td=""><td>QY 77 HENIVTLEDIXESTTHYXLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHE 136 </td></kir).>	QY 77 HENIVTLEDIXESTTHYXLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHE 136
F; 29	93-299/Region: autoinhibitory 02-314/Region: calmodulin binding 77/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicte	Qy 137 NGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAOKPY 196
Wa.	uery Match 45.9%; Score 1152.5; DB 1; Length 370; est Local Similarity 55.8%; Pred. No. 9.2e-44; atches 239; Conservative 46; Mismatches 62; Indels 81; Gaps 9;	197 SKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICH
Qy Db	12 WKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLFGKLFALKCI-KKSPAFRDSSLENEIA 70	196 GRAVDVMSIGVIALILLAGGIFFFIDESDANLERQIINGBIEFDAFINAGISGSANDFILM 257 LLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVHH :
Q Dp	71 VLKKIKHENIVTLEDIXESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSA 130 	236 LWCCDFEARFICQDAEDRFWIDGNIATINDINGIVAVHUANDLANGAMANANANANANANANANANANANANANANANANANA
Qy Db	131 VKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMBONG-IMSTACGTPGYVAPE 189	Db 318 LOMLRLSSNSNRLQKQASQOQPE 340 RESULT 4
oy Db	190 VLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISES 249	B88640 protein K07A9.2 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-Aug-2001
Qy	250 AKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFN 309	C; Accession: B88640 R; Anonywous, The C: elegans Sequencing Consortium. R; Anonywous, The C: elegans Sequencing Consortium. Science 282, 2012-2018, 1998 A; Title: Genome sequence of the nematode C: elegans: a platform for investigating bio
οy	310 AAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVLDHSVALPA 369	A.Reference number: A/5000; MUID:99069613; PMID:9631916 A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_

```
C; Species: Fugu rubripes
C; Species: Fugu rubripes
C; Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 03-Jun-2002
C; Accession: T30814
R; Cottage, A.J.; Clark, M.; Hawker, K.; Umrania, Y.; Wheller, D.; Bishop, M.; Elgar, FEBS Lett. 443, 370-374, 1999
A; Title: Three receptor genes for plasminogen related growth factors in the genome of A; Reference number: Z20880; MuID:99148833; PMID:10025966
A; Accession: T30814
A; Reference rubriminary; translated from GB/EMBL/DDBJ
A; Residues: 1-421 <COT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: AJ010348; NID:e1355080; PID:e1355083; PIDN: CAA09101.1 C; Genetics: A; Introns: 32/2; 76/2; 101/2; 147/3; 186/1; 211/2; 257/1; 283/2; 312/3
                                                                                                                             :|||||::||| : :|| | : ::| | |:|:|| | | ::| | | |:||||| | XWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFAR 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 AKWKKAVRVTTLMKRLR-----GAA 346
                                                                                                                                                                                                                                                                                                                                                                                                                   347 GGAVAAAAGGAAPASGASATVGTGGDAGCAAKSDDMASADRSATPATDGSATPATDGSVT 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PMHQGSLAAGPCGCCSSCLN----IGSKGKSSYCSEPTLLKKANKKQNFKSEVMV---PV 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 IYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 PENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPYSKAVDCWSI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||:| ::|||:||:|||:|||:|||1|:|||1|:|||1|:|||1|:|||1|:|||1|:|||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:|||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:||1|:|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 VVGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSP 250
                                                                                   FWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAK 301
                                                                                                                                                                                                                    SKWRQAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVL 361
                                                                                                                                                                                                                                                                                                                                                    ---RSLNCLVNGSL--HISSSLV 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVHHM 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKLHM-NLHSPGVRPEVENRPPETQASETS-RPSSPEITITEAPVLDHSVALPALTQLPC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 QVVKSEEFCEIFRAKDRNTLKMYTCKKFNKKDGRKVRKAAKNEIMILKMVKHHNILQLVD 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 EVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFR-DSSLENEIAVLKKIKHENIVTLED 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 28.0%; Score 703; DB 2; Length 42 Best Local Similarity 38.4%; Pred. No. 3.8e-24; Matches 154; Conservative 83; Mismatches 138; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calmodulin-binding protein kinase - Fugu rubripes
                                                                                                                                                                                                                                                                                                                                                 362 DHSVALPALTQLPCQHGRRPTAPGG-------
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IS6542

calmodulin-binding protein - rat
C:Species: Ratus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Sep-1999
C;Accession: I56542
R:Godbout, M.; Erlander, M.G.; Hasel, K.W.; Danielson, P.E.; Wong, K.K.; Battenberg, E.I.
J. Neurosci. 14, 1-13, 1994
A;Title: IG5: a calmodulin-binding, vesicle-associated, protein kinase-like protein enri
A;Recence number: I56542; MUID:94110847; PMID:8283228
A;Cression: I5642; MUID:94110847; PMID:828328
A;Accession: I5642; MUID:9410847; PMID:828328
A;Accession: I5642
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Wolecule type: mRNA
A;Residues: 1-504 < REE>
A;Cross-references: GB:L22557; NID:g349074; PIDN:AAa16633.1; PID:g349075
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
C;Reywords: calmodulin binding
F;22-286/Domain: protein kinase homology <KIN>
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A.Accession: B88640
A.Accession: B88640
A.Status: preliminary
A.Status: DNA
A.Residues: 1-310 <STO>
A.Residues: 1-310 <STO>
C.Genetics: A.Cross: references: GB:chr_IV; PIDN:AAC68810.1; PID:g3790765; GSPDB:GN00022; CESP:K07A9.C.Genetics: A.Gene: K07A9.2
A.Map position: 4
C.Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 AVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPE 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEIAVLK----KIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 AVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLS 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGT
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                                                                                                                                                                                                                                                                                                                                                                                Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  59; Indels
                                                                                                                                                                                                                                                                                                                                                                            Query Match 35.0%; Score 880; DB 2; Best Local Similarity 57.4%; Pred. No. 5.6e-32; Matches 159; Conservative 55; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KWRQAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPE 339
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N;Alternate names: Ca2+/calmodulin-dependent protein kinase Gr
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A; Residues: 1-37 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: 149571
A; Accession: 149571
A; Accession: 149571
A; Bitatus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 250-277, CFGI', 281-301, 'T', 303-338, 'X', 340-469 <RES>
A; Cross-references: GB:J03057; NID:g192366; PIDN:AAA37366.1; PID:g192367
A; Experimental source: brain
C; Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology
C; Keywords: alternative splicing; ATP; calmodulin binding; phosphotransferase; serine/tife; 460-266/Domain: protein kinase homology <KIN>
F; 460-266/Domain: protein kinase APP-binding motif
F; 306-466/Product: calspermin #status predicted <CSP>
F; 318-337/Region: calmodulin binding #status predicted
F; 71/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: mRNA
A; Residues: 1-469 <-300.
A; Cross-references: EMBL:X58995; NID:950366; PIDN:CAA41741.1; PID:950367
B; Sikela, J.M.; Hahn, W.E.
B; Sikela, J.M.; Hahn, W.E.
A; Sitela, J.M.; Hahn, W.E.
A; Sitela, J.M.; Hahn, W.E.
A; Recension acxpression library with a ligand probe: isolation and sequence of A; Reference number: A29878; MUID:87204263; PMID:3033675
A; Accession: A29878
A; Molecule type: mRNA
A; Residues: 315-469 <-SIK>
A; Molecule type: mRNA
A; Molecule type: mR
                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: cDNA sequence and differential expression of the mouse Ca(2+)/calmodulin-depend
A;Reference number: S17656; MUID:91372388; PMID:1893997
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                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S1766; A29878; 149571
K;Jones, D.A.; Glod, J.; Wilson-Shaw, D.; Hahn, W.E.; Sikela, J.M.
FEBS Lett. 289, 105-109, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 NCEYYFISPWWDEVSLNAKDLVKKLIVLDPKKRLTTFQALQHPWVTGKAANFVHMD---T 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 GIMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEET-ESKLFEKIK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTA--LHRDIYPS 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 469;
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                                                                                                                                  protein kinase (EC 2.7.1.123) IV
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42.7%; Pred. No. 7.2e-24;
11ve 60; Mismatches 121;
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                                                                                                                             Ca2+/calmodulin-dependent
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N; Contains: calspermin (Sorway rat) Aar-1993 #text_change 11-Jun-1999 (S; Species: Rattus norvegicus (Norway rat) C; Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 11-Jun-1999 (C; Accession: A41103; A41237; A32865; A41250; A32035; A60255; I53706 (C; Accession: A41103; A41237; A32865; A41250; A32000; N. B. Proc. Natl. Acad. Sci. U.S.A. 88, 5784-5788, 1991 (A) Title: Relationship of genes encoding Ca(2+)/calmodulin-dependent protein kinase Grangerence number: A41103; MUID:91288548; PMID:1648230 (A) AAccession: A41103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A. Molecule type: mRNA
A. Residues: 250-474 CoH3>
A. Cross-references: GB:104600; NID:g206172; PIDN:AAA41867.1; PID:g206173
A. Cross-references: GB:104600; NID:g206172; PIDN:AAA41867.1; PID:g206173
B. Mcans, A. R.; Cruzalegui, F.; LeMagueresse, B.; Needleman, D.S.; Slaughter, G.R.; On Mol. Cell. Biol. 11, 3960-3971, 1991
A. Title: A novel Ca(2+)/Calmodulin-dependent protein kinase and a male germ cell-spec A: Reference number: A41250; MUID:91304387; PMID:1649385
A. Accession: A41250
A. Molecule type: mRNA
A. Reference number: GB:M64757
B. Ono, T.; Slaughter, G.R.; Cook, R.G.; Means, A.R.
J. Biol. Chem. 264, 2081-2087, 1989
A. Title: Molecular cloning sequence and distribution of rat calspermin, a high affini A: Reference number: A32035; MUID:8912372; PMID:2914893
A. Accession: A32035
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A; Residues: 335-363 <0N2>
A; Note: the amino end of calspermin was blocked
B; Bland, M.M.
Gene 137, 351-352, 1993
A; Title: Identification of alternate 5' untranslated regions in the gene encoding Ca2
A; Reference number: 153706; MUID:94131312; PMID:8299971
A; Accession: 153706
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C;Superfamily: Ca2+(calmodulin-dependent protein kinase; protein kinase homology
C;Superfamily: Ca2+(calmodulin-dependent protein kinase homology arg. calmodulin binding; phosphotransferase; serine
F;40-296/Domain: protein kinase homology arkino-
F;40-296/Domain: protein kinase Arp-binding motif
F;48-57/Region: protein kinase Arp-binding motif
F;30-474/Product: calspermin #status predicted <CSP>
F;318-337/Region: calspermin binding #status predicted
F;71/Active site: Lys #status predicted
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C;Comment: Ca2+/calmodulin-dependent protein kinase IV is enriched in cerebellar gran
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A, Residues: 47-141, WE', 144-474 < OHI>
A, Cross-references: GB:M74488; NID:g203219; PIDN:AAA40845.1; PID:g203220
A, Note: this sequence has been revised in reference A41237
A, Note: part of this sequence was confirmed by sequencing of CDNA to mRNA
R; Ohmstede, C.A.; Bland, M.M.; Merill, B.M.; Sahyoun, N.
Proc. Natl. Acad. Sci. U.S.A. 88, 9375, 1991
A, Reference number: A41237
A, Molecule type: DNA
A, Residues: 142-143 < OH2>
A, Cross-references: GB:M63334
A, Note: this is a revision to the sequence from reference A41103
R, Note: this is a revision to the sequence from reference A41103
R, Dhanstede, C.A.; Jensen, K.F.; Sahyoun, N.E.
J, Blol. Chem. 244, 5866-5875, 1989
A, Title: Ca(2+)/calmodulin-dependent protein kinase enriched in cerebellar gr A, Reference number: A32865; MUID:89174647; PMID:2538431
A, Accession: A32865
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A;Residues: 306-371,'M',373-474 <ON1>
A;Cross-references: GB:J04446; NID:g203642; PIDN:AAA40990.1; PID:g203643
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Ca2+/calmodulin-dependent protein kinase IV beta polypeptide - rat
Cispecies: Rattus sp. (rat)
Cispecies: Rattus sp. (rat)
Cispecies: Rattus sp. (rat)
Cispecies: Accession: 152637
Risakagami, H.; Kondo, H.
Brain Res. Mol. Brain Res. 19, 215-218, 1993
A.Title: Cloning and sequencing of a gene encoding the beta polypeptide of Ca2+/calmodul
A.Reference number: 152637; MUID:94018484; PMID:8412563
A.Accession: 152637
A.Accession: 152637
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-502 CRES>
A.Cross-references: GB:S65840; MID:9425383; PIDN:AAB28372.1; PID:9425384
C.Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology
C.Keywords: ATP; calmodulin binding
F:68-334/Domain: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                          291 VSLQIQKNFAKSKWRQAFNA-----AAVVHHMRKLHMNLHSPGVRP-----EV 333
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                                                                                                                                                   115 YTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSK-MEQN 173
                                                                                                                                                                                                            AQKKLQEFNARRKLKAAVKAVVASSRLGSASSSHTNIQESNKASSEAQPAQDGKDKTDPL 368
                                                                                                                                 KKSPAFRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGV 114
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                                                                                     14 CSSVTSSTENLVPDYWIDGSKRDPLSDFFEVESELGRGATSIVYRCKQKGTQKPYALKVL 73
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                                                                 --IFMEV---LGSGAFSEVFLVKQRLTGKLFALKCI 54
                                                                                                                                                                                                                                                         174 GIMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEET-ESKLFEKIK
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   Length 474;
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27.6%; Score 692.5; DB 1;
40.8%; Pred. No. 1.2e-23;
live 62; Mismatches 120;
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Pred. No. 1.3e-23;
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                                   Conservative
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Matches 158
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Advoin-light-chain kinase (EC 2.7.1.117) A - slime mold (Dictyostelium discoideum)
N.Alternate names: MCCKA (EC 2.7.1.117) A - slime mold (Dictyostelium discoideum)
C.Species: Dictyostellum discoideum
A.Title: Characterization and bacterial expression of the Dictyostellum myosin light
A.Title: Characterization and bacterial expression of the Dictyostellum myosin light
A.Reference number: A40811; MUID:91340753; PMID:1651931
A.Reference number: A40811; MUID:91340753; PMID:1651931
A.Reference number: A40811
A.Reference number: A51816-13824, 1990
A.Reference number: 265, 18181-1824, 1990
A.Ritle: Dictyostellum myosin light chain kinase. Purification and characterization.
A.Recession: 265, 18181-1824, 1990
A.Ritle: Dictyostellum myosin light chain kinase. Purification and characterization.
A.Recession: 37125; MUID:90337997; PMID:2380188
A.Rocession: 371255
A.Rocession: A371255
A.Rocession: A371255
A.Rocession: A171255
A.Rocession: A1
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                                                                                                                                                                                                                   337 AQKKLQEFNARRKLKAAVKAVVASSRLGSASSSHTNIQESNKASSEAQPAQDGKDKTDPL 396
EGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTA--LHRDIYPS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 IKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                               DB 1; Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                        - AAVVHHMRKLHMNLHSPGVRP-
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50.2%; Pred. No. 8.7e-24;
tive 52; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ICHLLEKDPNERYTCEKALSHPWIDGNTA 282
                                                                                                                                                                                                                                                                                                                                   ENR-----PPETQASETSRPSSPEI 353
                                                                                                                                                                                                                                                                                                                                                                                                             ENKMOAGDHEAAKAAADETMKLQSEEV 423
                                                                                                                                                                        291 VSLQIQKNFAKSKWRQAFNA-
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nes 135; Conserv
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Cal-Y/calmodulin-dependent protein kinase (EC 2.7.1.123) - Emericella nidulans CiSpecies: Emericella nidulans, Aspergillus nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Species: O4.Dec.1992 #sequence_revision 04-Dec.1992 #text_change 21-Jul-2000
C;Accession: JN0323
R;Kornstein, L.B.; Gaiso, M.L.; Hammell, R.L.; Bartelt, D.C.
Gene 113, 75-82, 1992
A;Title: Cloning and sequence determination of a CDNA encoding Aspergillus nidulans c
A;Title: Cloning and sequence determination of a CDNA encoding Aspergillus nidulans c
A;Reference number: JN0323; MUID:9225350; PMID:1563634
A;Molecule type: mRNA
A;Residues: 1-414 KKOR>
A;Cross-references: GB:M/4120; NID:92804304; PIDN:AAB97502.1; PID:9168033
C;Comment: This protein has been implicated in cellular signal transduction and cell C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinase home.
C;Keywords: AfP: calmodulin binding: Phosphotransferase
F;21-37/Region: protein kinase AfP-binding motif
F;29-37/Region: calmodulin binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cispecies: Schizosaccharomyces pombe
Cispecies: Schizosaccharomyces pombe
Cispecies: Schizosaccharomyces pombe
Cispecies: Ob-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
Cispecies: T50290
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Cispecies: T50290
Cispecies: Schizosaccharomyces pombe
Cispecies: Schizosaccharomyces pombe
Cispecies: T50290

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQN--GIMSTACGTPGYVAPEVLAQKP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HMRKLHMNLHSPGVRPEVENRPP--ETQASETSRPSSPEITITEAPVL--DHSVALPALT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 KSLYRFGRTLGAGTYG---IVREADCSSGKVAVKIILKRNVRGNERMVYDELDLLQKLNH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 RKTFIFMEVLGSGAFSEVFLVKQR--LTGKLFALKCIKKSPAFRDSSLENEIAVLKKIKH 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 YSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 HILEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.9%; Score 651; DB 2; L
38.3%; Pred. No. 6.8e-22;
tive 78; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :| | | | | | : : | ::
----GNGE----SGGTKKRSLSKIARGAI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 QLPCQHGRRPTAPGG---RSLNCLVNGSL 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Matches 149;
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T50290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDLKPENLLYLTPEENSKIMITDFGLSK-MEQNGIMSTACGTPGYVAPEVLAQKPYSKAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 LDPKKRLTTFQALQHPWVIGKAANFVHMD---TAQKKLQEFNARRKLKAAVKA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.2%; Score 684; DB 1; 48.1%; Pred. No. 2.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53; Mismatches
  270
  242 IGKLLVVDVSKRLNATNALNHPWLKSNNS
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Matches 141;
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C: Accession: T23616
R:Wild, A.
Submitted to the EMBL Data Library, March 1996
A: Reference number: Z19771
A: Residues: 1-708 < WIL>
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C.Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                            415
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      RKEAYGKPVDIWACGVILYILLVGYPPFWDEDQHKLYQQIKAGAYDFPSPEWDTVTPEAK 246
                                                                                                      247 NLINQMLTINPAKRITAHEALKHPWVCQRSTVASMWHRQETVECLKKFNARRKLKGAILT 306
                                                                                                                                                                                                                      | : | | : | | : | 307 TMLATRNFSAA------KSLLNKKADGVKPQT-NSTKNSSAITSPKGSLPPAALESSDS 358
                                                                                                                                                                                                                                                                                                                                                                         397
                                                                                                                                                                                                                                                                                                                                                                                                                                      CGC------CSSCLNIGSKGKSS------YCSEPTL---LKKANK 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 PPCLSPGLLGPLPTPSPRISDILNSVRRGSGTPEAEGLPPVGPPPCPSPTLPGPLPTPSR 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKPENLLYLTPEENSKIMITDFGLS-KMEQNGIMSTACGTPGYVAPEVLAQKPYSKAVDC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNF-AKSKWRQAFNAAAVVHHMRKLH 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
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                                                               DFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNF-AKSKWRQA---
                                                                                                                                                                                                                                                                                                         356 TEAPVLDHSVALPALTQLPCQHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGP
                                                                                                                                                                                                                                                                                                                                                                      359 TNTTIEDEDAKAPRISDI------LNSVRRG-----CGTPEAEGPLSVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 MEVLGSGAFSEVFLVKQRLTGKLFALKCI -- KKSPAFRDSSLENEIAVLKKIKHENIVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein K11E8.1c - Caenorhabditis elegans
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S68470
Ca2+/Calmodulin-dependent protein kinase (EC 2.7.1.123) II beta-3 - rat
Ci2pedies: Rattus norvegicus (Norway rat)
C; Decides: Rattus norvegicus (Norway rat)
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 18-Jun-1999
C; Accession: S68470; I53501
R; Urquidi, V.; Ashcroft, S.J.H.
FEBS Lett. 358, 23-26, 1995
A; Title: A novel pancreatic beta-cell isoform of calcium/calmodulin-dependent protein ki
A; Reference number: I33501; MUID:95121451; PMID:7821422
A; Molecule type: mRNA
A; Residues: 1-589 cNRQ>
A; Molecule type: mRNA
A; Residues: 1-589 cNRQ>
A; Complex: heteromultiner composed of 10-12 chains (alpha, beta, gamma, delta) generally
C; Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology
C; Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology
C; Superfamily: Ca2+/calmodulin binding motif
F; 20-28/Region: protein kinase ATP-binding motif
F; 20-18/Region: protein kinase ATP-binding motif
F; 21.743,611,136,138/Active site: Lys, Glu, Asp, Lys #status predicted
F; 287,306/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted
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                                                            Length 335;
                                                                                                                   56; Mismatches 104; Indels
                                                         Score 630; DB 2;
Pred. No. 4.6e-21;
                                                         25.1%; Score 630; 43.6%; Pred. No. 4
A; Introns: 55/2; 73/3; 104/1; 214/2
                                                                                                                      Conservative
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Matches 158; Conservative
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Matches 133;
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Search completed: March 14, 2003, 14:10:05 Job time : $21\ \mathrm{secs}$

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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nucleic search, using sw model OM nucleic

March 14, 2003, 14:07:45; Search time 181 Seconds Run on:

(without alignments) 9488.751 Million cell updates/sec

Title: Perfect score:

US-09-960-643-1 2447 1 tggagtgggagctcaagcag......ttttctctaaaaaaaaa 2447 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1002604 Total number of hits satisfying chosen parameters: 501302 segs, 350932545 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_NA:*

1: /cgnn_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/USO0_NUW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 4, Appli		1,	1, 7	3,	7, 1	9	٠,				Sequence 49, Appl	Sequence 50, Appl	Sequence 189, App	Sequence 7777, Ap	Sequence 6, Appli	Sequence 3, Appli	7	H
Q1	US-09-935-464-4	US-09-935-464-2	US-09-935-464-1	US-10-024-036B-1	US-10-024-036B-3	US-09-935-464-7	US-09-835-788A-6	US-09-935-464-46	US-09-935-464-47	US-09-817-181-1	US-09-935-464-48	US-09-935-464-49	US-09-935-464-50	US-09-764-868-189	US-09-796-692-7777	US-09-935-464-6	US-09-797-039-3	US-09-797-039-1	US-10-153-921-1
DB	6	6	6	6	σ	6	10	9	6	10	6	6	6	6	σ	σ	10	10	12
% Query Match Length DB	1738	1383	157875	1772	1074	501	1578	480	467	1372	470	356	319	476	474	386	1503	2297	3124
% Query Match	70.9	54.7	37.0	20.6	20.5	20.4	20.3	19.6	17.7	17.7	16.9	13.2	13.0	11.9	10.9	10.0	10.0	10.0	10.0
Score	1734.8	1339.6	905.6	504.6	502.2	499.4	497	479	434.2	432.4	412.6	324.2	319	291	266.2	244.8	243.6	243.6	243.6
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Sequence 201, App Sequence 1, Appli Sequence 82, Appl	Sequence 3, Appli Sequence 5, Appli Sequence 4, Appli	Sequence 1, Appli Sequence 227, App Sequence 302, App Sequence 522, App		Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 177, App	Sequence 1537, Ap Sequence 20, Appl Sequence 6, Appli Sequence 8, Appli Sequence 10, Appl Sequence 210, App
9 US-09-764-868-201 9 US-10-116-332-1 9 US-10-001-835-82	10 US-09-992-481-3 10 US-09-992-481-5 9 US-10-024-036B-4	12 US-10-096-960-1 12 US-10-044-090-227 10 US-09-969-708-302 10 US-09-954-456-522	_	55 5	10 US-09-917-800A-1537 9 US-09-988-462-20 10 US-09-940-921B-6 10 US-09-940-921B-8 10 US-09-925-299-210
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ALIGNMENTS

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Sequence 4, Application US/0993464

Publication No. US20030027153A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin,
APPLICANT: Barrington-Martin,
APPLICANT: BARRING NETHOOS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSY:
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 332/14/102 US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT APPLICATION NUMBER: US/09/757,300
PRIOR PILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 90
SSOFTWARE: PALENTH VERSION 3.0
SSOFTWARE: PALENTH: 1738
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99.9%; Pred. No. 0;
live 0; Mismatches
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Matches 1736; Conservative
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ORGANISM: Homo sapiens
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US-09-935-464-4
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TCAAGCATGAAAACATTGTGACCCTGGAGGACATCTATGAGAGCACCACCCAC	ATCAGAATGGCATCGTCCACAGACTTAAAGCCCGAAAACCTGCTTTACCTTTACCCTTG	CCTACAGCAAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACC	ACTATGAGTTTGAGTCTCCGATTCTGGGATGAC	CCTGGATTGACGGAAACACGGCCCTCCACCGGGACATCTACCCATCAGTCAG	ACCACATGAGGAAGCTACACATGAACCTGCACAGGCCCGGGGGTCCCCCCACAGGTGGAGA	TCACCGAGGCACCTGTGCTGGACCAGTGTAGCACTCCCTGCCCTGACCCAATTACCCT	GCTCCTCCACATCAGCAGCAGCCTGGTGCCCATGCATCAGGGGTCCCTGGCCGCGGCCCGGGCCGGCC
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APPLICANT: Meyer, Joanne
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
TITLE OF INVENTION: MEHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYC
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/1H702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
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                                                    DB 9; Length 1383;
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US-09-935-464-2
; Sequence 2, Application US/09935464
; Publication No. US20030027153A1
; GENERAL INFORMATION:
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PatentIn version 3.0
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US-09-935-464-2
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APPLICANT: Meyer, Joanne Applicant: Meyer, Joanne Applicant: Bartington-Martin, Rory
APPLICANT: Bartington-Martin, Rory
APPLICANT: Barker, Alexander
TITLE OF INVENTION: BERORDERS SUCH AS SCHIZOPHRENIA
FILLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILLE REPERBNCE: 3322/14702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR APPLICATION NUMBER: US 09/757,300
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Pred. No. 2.7e-247;
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                                                                                                  Sequence 1, Application US/09935464 Publication No. US20030027153A1 GENERAL INFORMATION:
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Best Local Similarity .98.5%;
Matches 914; Conservative
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TYPE: DNA
                                                              RESULT 3
US-09-935-464-1
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                                          DD 148131 TCCAAAGTGGAATAGAAAGAAGTTCATGAGTAAGGGCTGCAAGGAATTCTTATCCTGGCC 148190
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) Fublication No. US20030028004A1
) GENERAL INFORMATION:
APPLICANT: Bandaru. Rajasekhar

TITLE OF INVENTION: 68730 and 69112, Protein Kinase

TITLE OF INVENTION: Molecules and Uses Therefor

FILE REFERENCE: MPI2000-521PIR(M)

CURRENT APPLICATION NUMBER: US/10/024,036B

CURRENT FILING DATE: 2001-12-17

PRIOR APPLICATION NUMBER: 60/258222

PRIOR APPLICATION NUMBER: 60/258222

PRIOR FILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 1

SEQ ID NO 1
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LOCATION: (169)...(1242)
EACTURE:
NAME/KEY: 3'UTR
LOCATION: (1243)...(1772)
FEATURE:
NAME/KEY: unsure
LOCATION: 1
LOCATION: 1
COTHER INFORMATION: n may be
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ORGANISM: Homo sapiens
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LOCATION: (1)...(168)
FEATURE:
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hes 695; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
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US-10-024-036B-1
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GGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAACAGACCACCAACAT 125

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GAACTITGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGCACCACAT 1019
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CCCGTTCTATGAAGAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGGGCTACTATGA
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; Sequence 3, Application US/10024036B
; Publication No. US20030028004Al
; GENERAL INFORMATION:
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|GAGAAACTACACCT 1139
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ACTCACTCCCACCTCTCAAGCCTCCAACCTCTTGGCCAGATTGGGCTCATTAATGTCGTT 2004
     Sequence 7, Application US/09935464 Publication No. US20030027153A1 GENERAL INFORMATION:
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SEQ ID NO 7
LENGTH: 501
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llarity 99.8%;
Conservative
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500; Conserv
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US-09-935-464-7
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APPLICANT: Bandaru, Rajasekhar TTLE OF INVENTION: 68730 and 69112, Protein Kinase TITLE OF INVENTION: Molecules and Uses Therefor FILE REFERENCE: MPI2000-521P1R(M) CURRENT APPLICATION NUMBER: US/10/024,036B PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2000-12-22
                                                                                     NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                        Best Local Similarity
Matches 692; Conserv
                                                                                                                        LENGTH: 1074
                                                                                                                                                        US-10-024-036B-3
                                                                                                                                    TYPE: DNA
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APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSY
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/1H702 US1
FUNERNY APPLICATION NUMBER: US/09/935,464
CURRENY APPLICATION NUMBER: US/09/935,464
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09 ö 1764 GATAGCTCTCGCCTGGGTCTGTGCTGTTTGTCGTGAAAGCTTAATGGGCTGGCCAGGCT 1884 TTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGCACCACATGAGG 1023 CAGAGGGAGGAAGGCAGAGCAAGTGGAGCAGGGCTTAGCAGGAGCAGTTTCTGGCCAGAA 1644 CCTGACCTGCCTGCTCTATGCCCCACACCCTACGTGCCGTGGCTCTGTGCAGTGTACGTA 1824 GTGTCACCTTCTCCAAGCAAAGCCATATGGAGCATCTACCCAGACTCCCACTCTGCACAC 1944 840 963 TITGCCAAGAGCAAATGGAGACAAGCATTTAATGCCACGGCCGTCGTGAGACATATGAGA 960 61 CAGAGGGAGGAAGGCAGAGCAAGTGGAGCAGGGCTTAGCAGGAGCAGTTTCTGGCCAGAA 120 Gaps CGTAGAAGCCTTGTTGAAGCTGTGAGCAGGAGAAGCGGTGCCCACCAGCTTCCAGGTCTC ó Length 501; Indels Score 499.4; DB 9; Pred. No. 1.2e-132; 0; Mismatches 1;

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Sequence 46, Application US/09935464

Publication No. US20030027153A1

GENERAL INFORMATION:
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYC
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/1H702 US1
CURRENT APPLICATION UNMBER: US/09/935,464
CURRENT APPLICATION NUMBER: US/09/935,464
PRIOR PELICATION NUMBER: US/09/935,464
PRIOR FILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-01-09
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OTHER INFORMATION: n=a or g or c or t/u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 90
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ORGANISM: Homo sapiens
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US-09-935-464-46
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US-09-935-464-46
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LENGTH: 480
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Matches 479;
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                                                                                                                                                                                                                               APPLICANT: Ni et al.
TITLE OF INVENTION: Death Domain-Containing Receptor Polynucleotides, Polypeptides,
TITLE OF INVENTION: Antibodies
FILE REFERENCE: P7018P1
CURRENT APPLICATION NUMBER: US/09/835,788A
CURRENT PILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-04-17
PRIOR PLICATION NUMBER: PC/129,585
PRIOR PLICATION NUMBER: 60/159,585
PRIOR APPLICATION NUMBER: 60/159,585
PRIOR APPLICATION NUMBER: 60/159,246
PRIOR FILING DATE: 1999-10-18
PRIOR PLILOR DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
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421 ACTCACTCCCACCTCTCAAGCCTCCAACCTCTTGGCCAGATTGGGCTCATTAATGTCGTT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385 TTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAGAAGGATGCCAGTCTGGTGATCCAG 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            622 TACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAGCAAGGCTGTGGATTGCTGGTCC 681
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Pred. No. 1.2e-131;
0; Mismatches 265; Indels
                                                                                                                                                                        Sequence 6, Application US/09835788A Patent No. US20020077458A1 GENERAL INFORMATION:
                                       2005 GCCTGCCCATCTGCATG 2025
                                                         481 GCCTGCCCATCTGCATGAATG 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 20.3%;
Best Local Similarity 71.6%;
Matches 682; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 1, Application US/09817181

Patent No. US2020142427A1

GENERAL INFORMATION:

APPLICANT: MERKULOV, Gennady et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REPERBENCE: CLOOL189

CURRENT APPLICATION NUMBER: US/09/817,181

CURRENT FILING DATE: 2001-03-27
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                                                         421 GTGAAATACCTACATGAGAATGGCATCGTNCACAGAGACTTAAAAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 196;
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Pred. No. 3.2e-113;
                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                    17.78;
73.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 563; Conservative
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                                                                                                                  RESULT 10
US-09-817-181-1
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                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
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                                                                                                                                                                                                                                                                                          Sequence 47, Application US/0993464

Publication No. US20030027153A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
BAPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA
TITLE OF INVENTION: US/090935,464
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
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                                                                                   CCTGGAAGAAACAGACCACCAACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGAT
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             TGTTGAAAAAGATCAAGCATGAAAACATTGTGACCCTGGAGGACATCTATGAGAGCACCA
                                                                                                                                AGCGGGGTGTCTACACAGAGAAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAG
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                                                                     CCCACTACTACCTGGTCATGCAGCTTGTTTCTGGTGGGGGAGCTCTTTGACCGGATCCTGG
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Best Local Similarity 96.4%; Pred. No. 5.1e-114;
Matches 450; Conservative 0; Mismatches 16;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 47
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OTHER INFORMATION: n=a or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                 RESULT 9
US-09-935-464-47
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APPLICANT: MONTH MARTIN, MONTH MONTH MONTH MONTH MONTH MONTH MARTIN, ROLY APPLICANT: BARTINGTON-MARTIN, ROLY APPLICANT: BARTING MARTIN, ROLY APPLICANT: BARTING MARCHAND MARCHAIL MARCHAND MARCH
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APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrer, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYC
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REPERBENCE: 3222/1H702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
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Pred. No. 1.2e-82;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc_feature
; OTHER INFORMATION: n=a or g or c or t/u
US-09-935-464-49
                                                                                                 Sequence 49, Application US/09935464
Publication No. US20030027153A1
GENERAL INFORMATION:
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98.0%;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 49
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ORGANISM: Homo sapiens
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US-09-935-464-50
                                                                              US-09-935-464-49
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APPLICANT: Meyer, Joanne
APPLICANT: Barrington Martin, Rory
APPLICANT: Barrington Martin, Rory
TITLE OF INVENTION: DISCROBERS SUCH AS SCHIZOPHRENIA
TITLE OF INVENTION: DISCROBERS SUCH AS SCHIZOPHRENIA
TITLE REPERENCE: 3322/11702 USJ
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PHIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-09
NUMBER OF SEQ ID NOS: 90
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CCATCAGTCAGCCTCCAGATCCAGAAGTTTGCTAAGAGCAAGTGGAGGCAAGCCTTC
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                                                                                                                                                                          Query Match 16.9%; Score 412.6; DB 9;
Best Local Similarity 96.2%; Pred. No. 7.7e-108;
Matches 452; Conservative 0; Mismatches 14;
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; OTHER INFORMATION: n=a or g or c or t/u
US-09-935-464-48
                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/09935464 Publication No. US20030027153A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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SEQ ID NO 48
LENGTH: 470
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                                                                                                                                                                                                                                                                                                   61 CCTGGAAGAAACAGACCACCAACATCGGAAAACCTTCATTTTTATGGAAGTGCTGGGAT 120
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                                                                                                                                                                                                                                                                                101 CCTGGAAGAAACAGACCACCAACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGAT 160
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 189
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                                                                                                                            Length 319;
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Patent No. US2020168711A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232

CURRENT APPLICATION NUMBER: US/09/764,868

CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                   0; Indels
                                                                                                                              Query Match 13.0%; Score 319; DB 9; 1
Best Local Similarity 100.0%; Pred. No. 3.6e-81;
Matches 319; Conservative 0; Mismatches 0;
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-189
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SOFTWARE: Patentin version 3.0 SEQ ID NO 50
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ORGANISM: Homo sapiens
                                                      TYPE: DNA
CRGANISM: Homo sapiens
US-09-935-464-50
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Best Local Similarity
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LOCATION: (59)
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US-09-764-868-189
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US-09-796-792-7777, Application US/09796692

Sequence 7777, Application US/09796692

GENERAL INFORMATION:

APPLICAMT: Adjact Paul A.

APPLICAMT: ADJACT PAUL ALIBORY PAUL CALING CONTON TO COURRET PELING DATE: 2001-03-01

PRIOR PELING DATE: 2000-03-17

PRIOR PELING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200, 393

PRIOR PELING DATE: 2000-04-28

PRIOR PELING DATE: 2000-04-28

PRIOR PELING DATE: 2000-05-04

PRIOR PELING DATE: 2000-06-04

PRIOR PELI
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Pred. No. 5.8e-66;
0; Mismatches 121;
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; OTHER INFORMATION: n=A,T,C or
US-09-796-692-7777
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Best Local Similarity 73.8%;
Matches 350; Conservative
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (10)
OTHER INFORMATION: n=A,T,C OI
OTHER INFORMATION: (19)
OTHER INFORMATION: 0
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US-09-796-692-7777/c
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Search completed: March 14, 2003, 17:30:10 Job time: 415 secs

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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1282 base pairs
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MEDIUM TYPE: Diskette
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Sequence 1,
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             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-459-448A-20
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US-08-459-444-26
US-09-547-26
US-09-547-801-3
US-09-467-082-3
US-09-347-801-3
US-09-930-181-1
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US-09-091-058-1
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TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN TITLE OF INVENTION: KINASES NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive Sequence 12, Application US/08878989 Patent No. 5885803 GENERAL INFORMATION: APPLICANT: Bandman, olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi

CITY: Palo Alto

DOS for Windows Version 2.0 OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ for Windows Vers CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/878,989 FILING DATE: COMPUTER: IBM Compatible CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0321 US
TELECHONE: 415-855-0555

TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear

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US-09-272-796-12
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                                                                      3;
                                          Length 1282;
                                                                    Indels
                                          Score 418; DB 2; I
Pred. No. 2.8e-109;
0; Mismatches 326;
                                        Query Match
Best Local Similarity 65.5%;
Matches 626; Conservative
; CLONE: 827431
US-08-878-989-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 CCACTACTACTGGTCATGCATGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGA 401
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llarity 65.5%; Pred. No. 2.8e-109;
Conservative 0; Mismatches 326;
                                                                                                                                                                                                   TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                      .: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FASTESE (FOR WINDOWS VERSION
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
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Sequence 12, Application US/09272796 Patent No. 6207148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                         APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 12:
                                                                                               APPLICANT: COFIEY, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1282 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                          GENERAL INFORMATION:
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IMMEDIATE SOURCE:
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FEATURE
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                  511
                                            461
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                                                                                                             582 ACAGAATGGCATCATGTCCACTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCT 641
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                                                                                                                                                                                                                                                                                                             702 ATTGCTCTGTGGATACCCCCCGTTCTATGAAGAAACGGAGTCTAAGCTTTTCGAGAAGAT 761
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522 CCTTACCCCTGAAGAGAACTCTAAGATCATGATCACGACTTTGGTCTGTCCAAGATGGA
                                                      882 CTTGAGTCATCCCTGGATTGACGGAAACACGGCCCTCCACCGGGACATCTACCCATCAGT
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                                                                                            462 GAAATACCTACATGAGAATGGCATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTA
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Edwards, Jean-Baptiste APPLICANT: Duelert, Aymeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 89, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
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STATE: California
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STREET: 501
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APPLICANT: WEI, Ming-Hui
APPLICANT: DIFRANCESCO, Valentina
APPLICANT: YAN, Chunhua
ITILE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILLE PERPENCE: CLOO0612
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Pred. No. 1.5e-86;
1; Mismatches 0
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CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 362 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
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Best Local Similarity 99.7°
Matches 337; Conservative
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US-08-715-568A-2
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                                                                                                                                                                                                               229 ATCAAGAAGTCACCTGCCTTCCGGGACAGCAGCCTGG---AGAATGAGATTGCTGTGTTG 285
                                                                                                                                                                                                                                                                                                                 346 TACTACCTGGTCATGCAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGG 405
                                                                                                                                                                                                                                                                                                                                                                 GGTGTCTACACAGAGGAAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAA 465
                                                                                                                                                                                                                                                                                                                                                                                         553 GGCTACTACTCGGAGCGAGCACACAAGCAACGTGGTACGGCAAGTCCTGGAGGCCGTGGCC 612
                                                                                                                                                                                                                                                                                                                                                                                                                  TACCTACATGAGAATGGCATCGTCCACAGAGCTTAAAAGCCCGAAAACCTGCTTTACCTT 525
                                                                                                                                                               169 TTCTCAGAAGTTTTCCTGGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGC 228
                                                                                                                                                                                                                                                                                                                              526 ACCCCTGAAGAGAACTCTAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAG
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                                                                                                               Length 3124;
                                                                                                             Score 243.6; DB 4;
Pred. No. 2.6e-59;
0; Mismatches 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     706 CTCTGTGGATACCCCCGTTCTATGAAGAAACGGAGTCT----
                         4.0
           NUMBER OF SEQ ID NOS: 3
SOFWARE: FastSEQ for Windows Version
SEQ ID NO 1
LENGTH: 3124
                                                                                                              10.0%;
58.5%;
PRIOR FILING DATE: 2000-05-30
                                                                                                              Query Match 10.0
Best Local Similarity 58.5
Matches 498; Conservative
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                                                            TYPE: DNA ORGANISM: HUMAN
                                                                                     US-09-734-030-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 CTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCACCTGCCTTCCGGGACAGCAGCC
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                                                                                                                                                                                         ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,568A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 197.2; DB 2;
Pred. No. 4.8e-46;
0; Mismatches 348;
                                        GENERAL INFORMATION:
APPLICANT: Brydz, Hans Peter Blankenborg
APPLICANT: Brede, Gaute
TITLE OF INVENTION: PSKH-1 Ribozymes and Uses
TITLE OF INVENTION: Treatment
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORSK 3.0-002
                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
; Sequence 2, Application US/08715568A; Patent No. 5856463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FOLGY, Shawn P.
REFERENCE/DOCKET NUMBER: FORS
TELECOMMUTICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEPHAX: 908-654-7866
                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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nilarity 54.3%;
Conservative 0
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                         ZIP: 07090-1497
COMPUTER READABLE FORM:
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643 GCCCAGAAACCCTACAGCAAGGCTGTGGATTGCTGGTCGATCGGCGTCATCACTACATA 702
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                                                                                                                                                                                                                                                  AAGGAGGCTACTATGAGTTTGAGTCTCCCATTCTGGGATGACATTTCTGAGTCAGCCAAG 822
                                                                                                                                                                                                                                                                                                              GACTITATTTGCCACTTGCTTGAGAAGGATCCGAACGAGCGGTACACCTGTGAGAAGGCC 882
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529 CCTGAAGAGAACTCTAAGATCATGATCACGACTTTGGTCTGTCCAAGATGGAACAGAAT 588
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APPLICANT: AKIRA, SHIZUO
APPLICANT: KAMAN, TARO
TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
FILE REPERENCE: PH-569
CURRENT APPLICANTION NUMBER: US/09/159,385
CURRENT FILING DATE: 1998-09-23
EARLIER FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 8
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Pred. No. 1.6e-36;
0; Mismatches 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09159385 Patent No. 5958748
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ilarity 55.3%;
Conservative (
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ORGANISM: Homo sapiens
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; LOCATION: (94)..(1455)
US-09-159-385-3
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Best Local Simi
Matches 361;
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US-09-159-385-3
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APPLICANT: YE, Jane et al.
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE REPERENCE: CL001158
CURRENT APPLICATION NUMBER: US/09/800,960
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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                                                                          TACTACAGTGAAGCAGTGCCAGCCACTGTATACATCAGATTCTGGAGAGTGTTAACCAC 490
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                                                                                                                         GCTGGTCCATCGCCGTCATCACCTACATATTGCTCTGTGGATACCCCCCGTTCTATGAAG 733
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 TIGGTCTGTC------CAAGATGGAACAGAATGGCATCATGTCCACTGCCTGTGGGA
                     AAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGGGCTACTATGAGTTTGAGTCTCCAT
                                                                                                                                                                                                                                                                                                             854 CGAACGAGGGGTACACCTGTGAGAAGGCCTTGAGTCATCCCTGGATTGACGGAAACACGG
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Pred. No. 5.2e-38;
0; Mismatches 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09800960
Patent No. 6387677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.9%;
Best Local Similarity 54.2%;
Matches 367; Conservative
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; ORGANISM: Human
US-09-800-960-1
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US-09-800-960-1
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NAME/KEY: CDS
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US-09-159-385-4
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                    515 AGCCGGAAAACATCATGCTGCTGGACAAGACGTGCCCAACCCACGAATCAAGCTCATCG
                                                                                                                                                                                                                                                                             AGCCCGAAAACCTGCTTTACCCTTACCCCTGAAGAG---AACTCTAAGATCATGATCACTG
                                                                            575 ACTICGGCATCGCGCACAAGATCGAGGCGGGGAACGAGTTCAAGAACATCTTCGGCACCC
                                                                                                                                                        677 GGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCCCCCCGTTCTATGAAGAAA
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                                                   ACTITIGGICTGICCAAGAIGGAACAGAAIGGCAICAIGICCACI ---GCCIGIGGGACCC
                                                                                                       CAGGCTACGTGCCTCCAGAAGTGCTGGCCCAGAAACCCTACAGCAAGGCTGTGGATTGCT
                                                                                                                                635 CGGAGTTTGTGGCCCCCAGAGATTGTGAACTATGAGCCGCTGGGCCTGGAGGCGGACATGT
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APPLICANT: AKIRA, SHIZUO

APPLICANT: KAWAI, TARO

TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE

FILE REPERENCE: 081356/0128

CURRENT APPLICATION NUMBER: US/09/186,277

CURRENT FILING DATE: 1998-11-05

EARLIER APPLICATION NUMBER: JP97/261589

EARLIER FILING DATE: 1997-09-26

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 8

SEQ ID NOS: 8
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Pred. No. 1.6e-36;
0; Mismatches 286;
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Best Local Similarity 55.3%;
Matches 361; Conservative 0
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; LOCATION: (94)..(1455)
US-09-186-277-3
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ORGANISM: Homo sapiens
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                           ACTICGGCATCGCGCACAGATCGAGGCGGGGAACGAGTTCAAGAACATCTTCGGCACCC
                                                                                                                                                                                                                      535 CGGAGTTTGTGGCCCCCAGAGATTGTGAACTATGAGCCGCTGGGCCTGGAGGCGGAGTATGT
                                                                                                                                                                                                                                                                 GGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCCCCCGGTTCTATGAAGAAA
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                                                                                                                                                                               CAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAGCAAGGCTGTGGATTGCT
                                                                                        ACTITIGGTCTGTCCAAGATGGAACAGAATGGCATCATGTCCACT - - - GCCTGTGGGACCC
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Patent No. 5958748
GENERAL INFORMATION:
APPLICANT: AIRA, SHIZUO
TITLE OF INVENTION:
FILE REFERENCE: PH-569
CURRENT FILING DATE: 1998-09-23
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: US/09/1261589
EARLIER PILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 8
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Pred. No. 1.3e-31;
0; Mismatches 297;
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53.6%;
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Best Local Similarity 53.63
Matches 350; Conservative
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ORGANISM: Mus musculus
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US-09-159-385-4
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ATGGCATCATGTCC---ACTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGG 643
                                                                                                                                  644 CCCAGAAACCCTACAGCAAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATAT 703
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                                                                                                                                                                                                                          ACTITATITIGCCACTTGCTTGAGAAGGATCCGAACGAGCGGTACACCTGTGAGAAGGCCT
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APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: SYNTHETIC DAWSEN OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOTER READABLE FORM:

COMPOTER READABLE FORM:

COMPUTER: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30B

APPLICATION DATA: US/O7/951,715A

FILING DATE: 25-SEP-1992
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Koziel, Michael G. APPLICANT: Desai, Nalini M. APPLICANT: Lewis, Kelly S. APPLICANT: Kramer, Vance C. APPLICANT: Warren, Gregory W. APPLICANT: Evola, Stephen V.
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Crossland, Lyle D.
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Merlin, Ellis J.
Launis, Karen L.
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CITY: Hawthorne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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US-07-951-715A-20
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APPLICANT:
APPLICANT:
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COUNTRY:
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                                                                                                                                                      TGCTCTGTGGATACCCCCCGTTCTATGAAGAACGGAGTCTAAGCTTTTCGAGAAGATCA 763
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                                                                                                                                                                                                                                                                                                                                            ACTITATITICCCACTIGCTIGAGAAGGAICCGAACGAGCGGIACACCIGIGAGAAGGCCT 883
   CCCCTGAAGAACTCTAAGATCATGATCACACTGACTTTGGTCTGTCCAAGATGGAACAGA 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 AGATCCGCCACCCCAACATCATAACACTGCATGACGTGTTCGAGAACAAGACAGATGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: AKIRA, SHIZUO
APPLICANT: KAWAI, TARO
TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
FILE REFERENCE: 081356/0128
CURRENT PAPLICATION NUMBER: 0590/186,277
CURRENT FILING DATE: 1998-11-05
EARLIER APPLICATION NUMBER: 1997-261589
EARLIER APPLICATION NUMBER: 1997-261589
EARLIER FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.0
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Best Local Similarity 53.6%;
Matches 350; Conservative
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; LOCATION: (10)..(1353)
US-09-186-277-4
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/note= "cDNA sequence for maize pollen-specific calcium dependent protein kinase gene as disclosed in Figure 30."
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: No. 5859336artis Corporation
STREET: Petent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ITITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.1e
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION NUMBER: US/08/459,448A FILING DATE: 02-UN-1995 CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/951,715 FILING DATE: 25-SEP-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/772,027 FILING DATE: 04-0CT-1991 ATTONEY/AGENT INFORMATION: NAME: Pace, Gary M. REGISTRATION NUMBER: 40403
Sequence 20, Application US/08459448A Patent No. 5859336
                                                                                                                                                        Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
                                                       Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
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                                                                                                                                                                                                                                                                                                                                   Pace, Gary M.
Suttie, Janet L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                 Dawson, John L.
Dunder, Erik M.
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STRANDEDNESS: single
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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ZIP: 10591-9005
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                    Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Koziel,
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                     /note= "cDNA sequence for maize pollen-specific calcium dependent protein kinase gene as disclosed in Figure 30."
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                                          S-18805/A/CGC 1577/CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 135.6; DB 1;
Pred. No. 1.1e-28;
0; Mismatches 294;
              REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-186
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEPHONE: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                       5.5%;
      Spruill, W. Murray
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Matches 312, Conservative
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OTHER INFORMATION:
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
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US-08-459-448A-20
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                                                                                           GATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAGAATGGC
                                                                                                                    153 GCCCCGCGGAGCTGCTCCGCCCATCGTGCAGATCGTGCACCTGCCACTCCATGGG
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CORRESPONDENCE ADDRESS:
ADDRESSER
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STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
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Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
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Dunder, Erik M.
Pace, Gary M.
Suttie, Janet L.
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/note= "cDNA sequence for maize pollen-specific calcium dependent protein kinase gene disclosed in Figure 30."
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                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
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51.5%; Pred. No. 1.1e-28;
iive 0; Mismatches 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3 TELECOMMUNICATION INFORMATION:
                                                                                                                                 CURRENT ARPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-UN-1995
CLASSIFICATION B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-5EP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTONNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
                                            : Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Pace, Gary M. REGISTRATION NUMBER: 40403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1349 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 51.5
Matches 312; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 3..1226
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                          OPERATING SYSTEM:
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10591-9005
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                                              MEDIUM TYPE:
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                     453 TTCTGGGCAGAGAACGAGAACGCATCTTCACCGCCATCCTGCGAGGCAGCTTGACCTC
                                                                                784 GAGTCTCCATTCTGGGATGACATTTCTGAGTCAGCCAAGGACTTTATTTGCCACTTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pace, Gary M. APPLICANT: Suttle, Janet L. TITLE OF INVENTION: SYMPHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INSCIICIDAL ACTIVITY IN MAIZE NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CG1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8887
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: No. 6075185artis Corporation
: 3054 Cornwallis Road
Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-5EP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/08459504B Patent No. 6075185 GENERAL INFORMATION: APPLICANT: Koziel, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
                                                                                                                                                                                                                                                                                                                                                                   Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
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COMPUTER READABLE FORM:
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ADDRESSEE: NO. 60751
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US-08-459-504B-20
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APPLICANT:
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/note= "cDNA sequence for maize pollen-specific calcium dependent protein kinase gene as disclosed in Figure 30."
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                                                                                                                                                                                                                                                            Length 1349;
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Pred. No. 1.1e-28;
0; Mismatches 294;
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51.5%;
                1349 base pairs
nucleic acid
MESS: single
                                                                                                                                                                                                                                                                              Best Local Similarity 51.5
Matches 312; Conservative
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        OTHER INFORMATION:
COTHER INFORMATION:
US-08-459-504B-20
                                                                                     CDNA
                                                                                                                                                       LOCATION: 3..1226
OTHER INFORMATION:
                                                                   linear
                                                                                MOLECULE TYPE: CE
HYPOTHETICAL: NO
FEATURE:
                                                                                                                                         NAME/KEY: CDS
                                TYPE: nucleic STRANDEDNESS:
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                                                                   TOPOLOGY:
                  LENGTH:
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664 GCTGTGGATTGCTGGTCCATCGCCGTCATCCTACATATTGCTCTGTGGATACCCCCCG 723
                                                                                                                                                                                                                   ITCTATGAAGAAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGGCCTACTATGAGTTT 783
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544 AAGATCATGATCACCACTTTGGTCTGTCCAAGATGGAACAGAATGGCATCATGTCCACT 603
                                                                       604 GCCTGTGGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAGCAAG
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Job time : 102 secs
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                                                                                                                                                                               ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                           INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED NUCLEIC ACID CODING SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 135.6; DB 3; Length 1349;
Pred. No. 1.1e-28;
0; Mismatches 294; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUTCATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFRAX: (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <UNKnOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/951,715
FILING DARE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DARE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 3..1226
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                 Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis, Launis, Karen L.
                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1349 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.5%;
Best Local Similarity 51.5%;
Matches 312; Conservative
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO FEATURE:
                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
                                                                                                                                                                                                                                      STATE: NC
COUNTRY: USA
                                                                                                                                                                                                                                                                       ZIP: 27709
                                                                                                             TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-459-444-20
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Run on:

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Sequence 19, Application US/08878989
; Sequence 19, Application US/08878989
; Patent No. 5885803
; GENERAL INFORMATION:
    APPLICANT: Bandman, Olga
    APPLICANT: Hillman, Jennifer L.
    APPLICANT: Guegler, Rari G.
    APPLICANT: Golly, Neil C.
    APPLICANT: Gall, Preeti
    APPLICANT: Gall, Surya K.
    APPLICANT: Shah, Purvi
    TITLE OF INVEWION: DISBASE ASSOCIATED PROTEIN
    TITLE OF INVEWION: KINASES
    NUMBER OF SEQUENCES: 21
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: INCYLE Pharmar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM 11FE: JEBA COMPUTER: COMPUTER: IBM COMPUTER: OPERATING SYSTEM: DOS SOCTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/878,989 FILING DATE: CLASSPICATION: 435 PRIOR APPLICATION 1435 APPLICATION NUMBER: FILING DATE: ATTORNEY/AGGNT INFORMATION: NAME: Billings, Lucy J J NAME: Billings, Lucy J J RESISTATION NUMBER: 36,740 COMPUTER ATTORNEY/AGGNT INFORMATION: NAME: Billings, Lucy J J RESISTATION NUMBER: 36,740 COMPUTER ATTORNEY/AGGNT NUMBER: MANORY NUMBER: 36,740 COMPUTER ATTORNEY/AGGNT NUMBER: MANORY NUMBER: MA
US-08-459-444-25
US-09-347-412-25
US-09-347-101-17
US-08-464-164-2
US-08-668-416-2
US-09-257-8258-2
US-09-257-8258-2
US-09-186-277-1
US-09-142-5518-2
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US-09-143-5518-2
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STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
2.1P: 94304
COMPITION
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US-07-857-224B-23
US-09-347-801-18
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
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        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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(without alignments)
875.332 Million cell updates/sec
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Sequence 14, Api
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-27-796-5
US-09-727-796-5
US-09-714-030-2
US-07-87-224B-18
US-07-857-224B-18
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US-09-960-2
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US-09-961-7158-23
US-07-821-7158-23
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US-08-459-448A-25
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5-09-272-796-19
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Maximum Match 100%
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TOPOLOGY: linear IMMEDIATE SOURCE:
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; CLONE: 790790
US-09-272-796-19
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US-09-457-040B-31
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                                                                                                                              10 W-KQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKEALEGKEGSMENEIA 68
                                                                           81; Gaps
                                                                                                           12 WKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIA 70
                                            Length 370;
                                                                             62; Indels
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APPLICANT: Bandman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Guegler, Karl G.
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                            DB 2;
                                          45.9%; Score 1152.5; DB illarity 55.8%; Pred. No. 1.5e-93; Conservative 46; Mismatches 62
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APPLICATION NUMBER: US/09/272,796
FILLING DATE:
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3174 Porter Drive
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/09272796 Patent No. 6207148 GENERAL INFORMATION:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                              Query Match
Best Local Similarity
Matches 239; Conserv
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US-08-878-989-19
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Patent No. 6387641
GENERAL INFORMATION:
APPLICANT: Vertex Pharmaceuticals Incorporated
APPLICANT: Bellon, Steve
TITLE OF INVENTION: Crystallized P38 Complexes
FILE REFERENCE: VPI/98 14
CURRENT APPLICATION NUMBER: US/09/457,040B
CURRENT FILING DATE: 1999-12-08
NUMBER OF SEO ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 31
LENGTH: 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.9%; Score 1152.5; DB 55.8%; Pred. No. 1.5e-93 tive 46; Mismatches 6
                                                                   \overline{0}
                                                                     PF-0321
                   NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPANE: 415-685-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 370 amino acids TYPE: amino acid STRANDEDNESS: single
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 55.8%
Matches 239; Conservative
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ADDRESSEE:
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US-09-272-796-5
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                                                                         Gaps
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                                                                         81;
                                            DB 4; Length 370;
                                                                        62; Indels
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APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 21
                                         45.9%; Score 1152.5; DB 55.8%; Pred. No. 1.5e-93; Live 46; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Bandman, Olga
: Hillman, Jennifer L.
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                     Best Local Similarity 55.89
Matches 239; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ADDRESSEE: Incyte PA
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 343;
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APPLICANT: COLLEY, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Gali, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.4%; Score 990; DB 2; 59.8%; Pred. No. 2.9e-79; Live 49; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                               PF-0321 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09272796 Patent No. 6207148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                        REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                      LENGTH: 343 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 59.8
Matches 193; Conservative
                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                 TELEFAX: 415-845-4166
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear IMMEDIATE SOURCE: LIBRARY: PROSNOT06 : CLONE: 827431 US-08-978-989-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 31/4 ... CITY: Palo Alto
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CURRENT APPLICATION NUMBER: US/09/734,030
CURRENT FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/207,281
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418 VTPVTDRSATP-----
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07090-1497
                                                                                                                                                   ; ORGANISM: HUMAN US-09-734-030-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-715-568A-1
                                                                                                   SEQ ID NO 2
LENGTH: 501
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                                                                                                                                    TYPE: PRT
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Sequence 2, Application US/09734030
Patent No. 6461846
GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen M.
APPLICANT: WETCHUM, Karen A.
APPLICANT: WET, Ming-Hui
APPLICANT: WET, Ming-Hui
APPLICANT: YAM, Chunhua
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO0612
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                              SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                    \mathbf{n}\mathbf{s}
                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF-0321
TELECOMNUMICATION HYPORMATION:
TELEPHONE: 415-855-0555
TELEPAS: 415-845-4166
                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 LFLRHIRKL-----GOIPEGE 320
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                                                                                                                                                                                                                                                                                                                               LENGTH: 343 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 5:
     IBM Compatible
                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                   PROSNOT06
 COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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; CLONE: 827431
US-09-272-796-5
                                                                                     FILING DATE:
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Best Local Simi
Matches 193;
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190 VLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETE-----SKLFEKIKEGYYEFESP 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 AKWKKAVRVTTLMKRLR------APEQSSTAAAQSASATDTATPGAAGGATAAAA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 ITITEAPVLDHSVALPALTQLPCQHGRRPTAPGGRSLNCLVNGSL--HISSSLVPMHQGS 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 AVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLS 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L-----AAGPCGCCSSCLNIGSKGKSSYCSEPTLLKKANKKQNFKSEVMV---PVKASG 461
                                                         Gaps
                                                                                                                15 QTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRD-----SSLENEI 69
                                                                                                                                            61;
     Length 501;
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STREET: 600 South Avenue West
CITY: Westfield
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08715568A
Patent No. 5856463
GENERAL INFORMATION:
APPLICANT: Prydz, Hans Peter Blankenborg
APPLICANT: Brede, Gaute
TITLE OF INVENTION: PSKH-1 Ribozymes and Uses in ITILE OF INVENTION: Treatment
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
Ouery Match 29.7%; Score 747.5; DB 4; Best Local Similarity 35.3%; Pred. No. 1.2e-57; Matches 173; Conservative 86; Mismatches 170;
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Score 592; DB 4;
Pred. No. 7.5e-44;
                         TELEFHONE: (International) 41 1 632 2830 TELEFAX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                   FEATURE: Protein kinase; Table 8 Column 26 PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                        AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNEL: Science
VOLUME: 241
           TELECOMMUNICATION INFORMATION:
                                                                                  24:
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Best Local Similarity 46.99
Matches 119; Conservative
                                                            TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 264
                                                                                                                                                                           MOLECULE TYPE:
DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | :|| |||:
248 ARMTALQALRHPWV 261
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                                                                                                                                       amino acid
                                                                                                                                                           linear
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ORGANISM: hum
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                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-857-224B-24
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                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                          PAGES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 ERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMN 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...---AASSSMKNLHRS 370
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        27 EVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRDSSLENEIAVLKKIKHENIVTLEDI 86
                                                                                                                                                                                                                                                                                                                                                                                                       35;
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Patent No. 5958784
GENERAL INFORMATION:
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
STATE: none
COUNTRY: Switzerland
                                                                                                                                                                                                                                                                                                                                                                 Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                       98; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,568A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGRNT INFORMATION:
NAME: FOLEY, Shawn P.
REPERENCE/DOCKET NUMBER: FORSK 3.0-002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             25.9%; Score 650.5; DB 2;
40.2%; Pred. No. 3.5e-49;
tive 62; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 ARMTALQALRHPWV-----VSM---
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 LHSPGVRPEVENRPPETQASETSRPS 349
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                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacInto
                                                                                                                                                                                                                                                                   ; LENGTH: 424 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-715-568A-1
                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 40.2
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-07-857-224B-24
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Sequence 4, Application US/09800960

Patent No. 6387677

GREERL INFORMATION:

APPLICANT: FE, Jane et al.

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REPERBNCE: CL001158

CURRENT APPLICATION NUMBER: US/09/800,960

CURRENT FILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastsEQ for Windows Version 4.0

SEQ ID NO 4 88 ESTTHYYLVWQLVSGGELFDRILERG-VYTEKDASLVIQQVLSAVKYLHENGIVHRDLKP 146 ENLLYLTPEENSKIMITDFGLSKMEQNG---IMSTACGTPGYVAPEVLAQKPYSKAVDCW 203 SIGVITYILLCGYPPFYEFTESKLFEKIKEGYYFFESPFWDDISESAKDFICHLLEKDPN 263 Gaps 8 LIGRGSFSRVVRVEHRATRQPYAIKMIETKYREGREVCESELRVLRRVRHANIIQLVEVF 67 28 VLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRDSSLENEIAVLKKIKHENIVTLEDIY 87 Length 556; 24.9%; Score 625; DB 2; Length 26 46.9%; Pred. No. 3e-47; iive 50; Mismatches 81; Indels

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FEATURE: Protein kinase; Table 8 Column
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                                                                                          252 DFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNF-AKSKWRQAFNA 310
                                                                                                                                                                                                                                                                                                       247 NLINQMLTINPAKRITADQALKHPWVCQRSTVASMWHRQETVECLRKFNARRKLKGAILT 306
                                                                                                                                                                                                                                                                                                                                                311 AAVVHH---MRKLHMNLHSP-GVRPEVENRPPETQASETSRPSSPEITITEAPVLDHSVA 366
                                                                                                                                                                                                                                                                                                                                                                              ----- 340
                                                                                                                                                                                                                                                                                                                                                                                                             367 LPALTQLPCQHGRRPTAPGGRSLNCLVNGSLHISSS-----LVPMHQGSLAAGPCGC 418
                                                                                                                                                                                                                                                                                                                                                                                                                               341 SPAQEPAPLQTAMEPQTTVVHNATDGIKGSTESCNTTTEDEDLKAAPLRTGNGSSVPEGR 400
                                                                                                                                                                           AQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAK 251
                                                                                                                                                         HENGIVHRDLKPENLLYLTPEENSKIMITDFGLS---KMEQNGIMSTACGTPGYVAPEVL 191
                                                             8 TRFTDDYQLFEELGKGAFSVVRRCVKKTSTQEYAAKIINTKKLSARDHQKLEREARICRL 67
                               17 TNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI--KKSPAFRDSSLENEIAVLKK 74
 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INTENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (International) 41 1 632 2830 TELEFAX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                              307 TMLVSRNFSAAKSLLNKKSDGGVKPQSNNK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 CSSCLNIGSKGKSSYCSEPTLLKKANKKQ 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 SSRDRTAPSAGMO---POPSLCSSAMRKQ 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple MacIntosh
OPERALING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Steven A. Benner
Hadlaubstrasse 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: none TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18:
 Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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Matches 149;
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APPLICANT: LOTTEN, Walter H.M.L.
APPLICANT: PARKER, Andrew E.
APPLICANT: MCGOMAN, Clare H.
APPLICANT: BLASINA, Alessandra
TITLE OF INVENTION: Human Checkpoint Kinase, hCDS1, Compositions and Methods
FILE REFERENCE: TSRI 649.0
CURRENT APPLICATION NUMBER: US/09/529,093A
CURRENT FILING DATE: 1998-10-21
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1997-10-22
NUMBER: OF SEQ 1D NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 -SPAFRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVWQLVSGGELFDRILERGVY 115 | | ::| | | ::| | ::| | | :|| | ::|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDL 144
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                                                                                                                                                                                                                                                                                                                                         27 EVLGSGAFSEVFLVKQRLTGKLFALKCI -- KKSPAFRDSSLENEIAVLKKIKHENIVTLE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 EELGKGAFSVVRRCVKVLAGQEYAAKIINTKKLSARDHQKLEREARICRLLKHPNIVRLH
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                                                                                                                                                                                                                                                    Length 264;
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.0%; Score 578.5; DB 4;
43.9%; Pred. No. 1.1e-42;
tive 47; Mismatches 91;
                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                    23.4%; Score 587.5; DB 2
46.6%; Pred. No. 6.2e-44;
tive 42; Mismatches 88
  PUBLAZ.
AUTHORS: Hanks, S. K.
AUTHORS: Hunter, T.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
""ALMB: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-529-093A-2; Sequence 2, Application US/09529093A; Patent No. 6413755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNERYTCEKALSHPWIDGNTALHR 285
                                                                                                                                                                                                                                                        Query Match 23.4%
Best Local Similarity 46.6%
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
PUBLICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                              US-07-857-224B-18
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US-09-529-093A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
LENGTH: 543
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Matches 126;
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Predicting Folded Structures of Proteins
                                                                                                                    STATE: none
COUNTRY: Switzerland
21P: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.4%; Score 564; DB 2;
45.7%; Pred. No. 7.3e-42;
tive 42; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (International) 41 1 632 2830 TELEFAX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE: Protein kinase, Table 8 Column 21 PUBLICATION INFORMATION:
                                                                                                                                                                                                        COMPOTER: Apple MacIntosh
COMPOTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION 436
PROOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
                                                                       ADDRESSEE: Steven A. Benner
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicti
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                     Hadlaubstrasse 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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PAKRITAHEALKHPWV 261
                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: Hanks, S. K. AUTHORS: Quinn, A. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                         ADDAR STREET: hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAGES: 42-52
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-857-224B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Sim
Matches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09800960
Patent No. 6387677
GENERAL INFORMATION:
ATHER OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREF
TITLE OF INVENTION: THEREF
CURRENT APPLICATION NUMBER: US/09/800,960
CURRENT FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                    175 IMSTACGTPGYVAPEVLAQ---KPYSKAVDCWSIGVITYILLCGYPPFYE-ETESKLFEK 230
                                                                                                                          DFICHLLEKDPNERYTCEKALSHPWIDGNTA----LHRDIYPS-------V 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | : | : | : | | : | | 306
247 NLINQMLTINPAKRITADQALKHPWYCQRSTVASAMHRQETVECLRKFNARRKLKGAILT 306
264 ADPAL --- NVETEIELKKLNHPCIIKIKNFFDA - EDYYIVLELMEGGELFDKVVGNKRL 319
                                116 TEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSK-MEQNG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 IKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HENGIVHRDLKPENLLYLTPEENSKIMITDFGLS---KMEQNGIMSTACGTPGYVAPEVL 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLQIQKNFAKSKWRQ-----AFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 RPSSPEITI-----TEAPVLDHSVALPALTQLPCQHGRRPTAPGGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                             231 IKEGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWI 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 22.7%; Score 571.5; DB 4; Best Local Similarity 34.4%; Pred. No. 4.9e-42; Matches 142; Conservative 69; Mismatches 151;
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Sequence 19, Application US/07857224B

Fatent No. 5958784

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Human
US-09-800-960-2
                                                                                                                                                                                                                                                                                US-09-800-960-2
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145 KPENLLYLTPEENSKIMITDFGLSKMEQNGIMST---ACGTPGYVAPEVLAQKPYSKAVD 201 202 CWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKD 261 27 EVLGSGAFSEVFLVKQRLTGKLFALKCI--KKSPAFRDSSLENEIAVLKKIKHENIVTLE 84 85 DIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDL Length 264; 91; Indels

3,

RESULT 14 US-07-951-715A-23

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202 CWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKD 261
                                                                                                                                           65 DSISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIHQILESVNHIHQHDIVHRDL 124
                                      145 KPENLLYLTPEENSKIMITDFGLS---KMEQNGIMSTACGTPGYVAPEVLAQKPYSKAVD 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                         244 PAKRITADQALKHPWVCQRSTVASMMHRQETVECLRKFNARRKLKGA 290
                                                                                                                                                                                                262 PNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNF-AKSKWRQA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESSS:
ADDRESSE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/459,448A FILING DATE: 02-JUN-1995 CLASSIFFFARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Pace, Gary M.
REGISTRATION NUMBER: CGC 1577/CIP/DIV4
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/08459448A Patent No. 5859336 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
Pace, Gary M.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
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Warren, Gregory W
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Lewis, Kelly S.
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US-08-459-448A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "rat protein kinase II
protein sequence as shown in Figure 32.
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                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
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41.8%; Pred. No. 9.5e-42;
iive 56; Mismatches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: SPIVILL, W. WLITRAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5-18805/A/(
TELECOMUNICATION INCRAFTION:
TELECOMUNICATION INCRAFTION:
TELECHONE: (919)541-8615
TELEFERAX: (919)541-8615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/951,715A FILING DATE: 25-SEP-1992 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIBA-GEIGY Corporation
Sequence 23, Application US/07951715A Patent No. 5625136 GENERAL INFORMATION:
                                                                                                                                     Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
                                                         Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                     Dawson, John L.
Dunder, Erik M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Clba-communerer: 7 Skyline Drive
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                                                                                                                                                                                                                                                                                                                                          Pace, Gary M.
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Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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; OTHER INFORMATION:
US-07-951-715A-23
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TTY: Hawthorne
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                                                                            /note= "rat protein kinase II
protein sequence as shown in Figure 32."
                                                                                                                    Query Match 22.4%; Score 563.5; DB 2; Length 295; Best Local Similarity 41.8%; Pred. No. 9.5e-42; Matches 120; Conservative 56; Mismatches 104; Indels 7
                                                                                                                                                                                                                                                                                                                                                        262 PNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNF-AKSKWRQA 307
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..295
OTHER INFORMATION: prot
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Search completed: March 14, 2003, 14:10:30 Job time : 19 secs

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Q9ynb8 gallus gall Q9y2h4 homo sapien Q00168 drosophila Q9v495 drosophila Q95559 gallus gall Q95266 sus scrofa

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095523 homo sapien
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2513
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               GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                    671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                   protein search, using sw model
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Match Length
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
Lunitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
Lunitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RemBL; ALO49688; CAB41259-11; "
RHSPP: 064450; 1A06.
InterPro; IPR001249; Euk_pkinase.
R InterPro; IPR001249; PRINT_Pkinase.
R InterPro; IPR001249; FYT_pkinase.
R Prints; PR00109; PKXRINASE.
R ProDom; PD0000001; Euk_pkinase; 1.
R PROSTITE; PS00109; PKRNYANISE.
R PROSTITE; PS00129; PRENYLATION; UNKNOWN 1.
R PROSTITE; PS0011; PROTEIN_KINASE_DOM; PROSTITE; PS0011; PROTEIN_KINASE_DOM; PROSTITE; PS0011; PROTEIN_KINASE_DOM; I.
R PROSTITE; PS00108; PROTEIN_KINASE_DOM; I.
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                                                                               01-NOV.1999 (TrEMBLrel. 12, Created)
01-NOV.1999 (TrEMBLrel. 12, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 53.6 kDa protein (Fragment).
Hypothetical F3.6 kDa protein (Fragment).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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481 AA
PRT;
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Matches 476; Conservative
PRELIMINARY;
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Q9nny2 homo sapien Q9txjO caenorhabdi Q9uah6 caenorhabdi Q9v3i4 drosophila Q8wtt8 homo sapien Q9bqc9 homo sapien

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53128 MW;
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                                                                                                       Conservative
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Best Local Similarity
476 AA;
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                                                                             Similarity
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                                                                             Best Local Sim
Matches 474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 RDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVWQLVSGGELFDRILERGVYTEKDA 125
                                                                                                                                                                                                                     SLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTAC 180
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                                                                                                       RDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDA 120
                         MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAF
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Characterization of the human ortholog of rat CaM Kinase I (Camirig) at 1932-941.";
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF428261; AAL28100.1; -.
InterPro; IPR000719; ENE_pkinase.
InterPro; IPR00130; Prenyl_site.
InterPro; IPR001290; Ser_thr_pkinase.
InterPro; IPR001290; Ser_thr_pkinase.
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Q96NX5;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
Calcium/calmodulin-dependent protein kinase I gamma.
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SMART: PR0011; Euk_pkinase; 1.
SMART: PR0011; TYRC: 1.
PROSITE: PS00294; PRENYLATION; UNKNOWN_1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Transferase.
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SEQUENCE FROM N.A.
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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AL023754; CAA19296.1; -.
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                                         Length 476;
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DD0AEAA016E7506E CRC64;
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Primates; Catarrhini; Hominidae;
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01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
DJ272L16.1 (Rat Ca2+/calmodulin dependent protein k
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Pred. No. 1.9e-178;
                                     9; DB 4;
4.8e-190;
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                                                                                2; Mismatches
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002299; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
PR051TE; S000200; S. TKC; 1.
PR051TE; PS00107; PR0TEIN_KINASE_DOM; 1.
PR051TE; PS001108; PROTEIN_KINASE_DOM; 1.
PR051TE; PS001108; PROTEIN_KINASE_DOM; 1.
ATP-binding; Serine/threonine-protein kinas
                                       99.8%; Score 2509; 99.6%; Pred. No. 4.8
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
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InterPro; IPR001245; Tyr_pkinase.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 20, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
BM106NZ3.1 (Novel protein kinase (Ortholog of human dJ272L16.1 and rat Ca2+/calmodulin dependent protein kinase)
(Calcium/calmodulin-dependent protein kinase I gamma) (Hypothetical 53.3 kDa protein).
BM106NZ3.1 OR CANKIG.
Mus musculus (Mouse).
                                                                                                                                        PFWDDISESAKDFICHLLEKDPNERYTCEKALSHDWIDGNTALHRDIYPSVSLQIQKNFA 300
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                                                               MGRKEEDDCSSWKKQTINIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAF 60
                                                                                                                                                                                                                                                                                 GTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFES
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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      Indels
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EMBL; AL365314, CAC41399.1; -.
EMBL; AR428262; ABL28101.1; -.
EMBL; EC021840; AAH21840.1; -.
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    Mismatches
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INTECFPO; IPR000719; EU&_Psinase..
INTECFPO; IPR001230; Persyl_site.
InterPro; IPR002290; Ser_thr_pkinase.
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Submitted (OCT-2001) to
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447;
    Matches
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SLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTAC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein Kinase (Fragment).
Rattus norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Yokokura H., Terrada O., Naito Y., Hidaka H.;
"Isolation and comparison of rat cDNAs encoding Ca2+/calmodulin-dependent protein kinase I 1906rms.";
Biochim. Biophys. Acta 1338:8-12(1997).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL. BA6557; BAA19880.1; -.
HSSP; Q63450; 1A06.
InterPro; IPR000729; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                      DB 11; Length 477;
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                                                                                                                                                                                                                                                                   92.6%; Score 2327.5; DB 11; Lengt
92.0%; Pred. No. 1.1e-175;
Live 14; Mismatches 23; Indels
Pfam; PF00069; pkinase; 1.

Prodom; PD000001; Euk_pkinase; 1.

PROSITE; SM00219; TYRC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

ATP-binding; Kinase; Transferase; Hypothetical protein.

SEQUENCE 477 AA; 53296 MW; 3A61FBDC49A7BB56 CRC64;
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Last annotation update)
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MEDLINE=97228532; PubMed=9074610;
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                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                       al Similarity
439; Conserv
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us-09-960-643-2.rspt

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FAKSKWRQAFNAAAVVHHMRKLHM 322
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          49.6%;
ilarity 73.1%;
Conservative 40
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Matches 222; Conservative
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            Query Match
Best Local Similarity
Matches 237; Conserv
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Q91YS8;
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                                                                                                                                                                                               Gaps
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"Identification and characterization of CKLik: a novel granulocyte
Ca2+/calmodulin-dependent kinase.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                              Query Match 64.1%; Score 1612; DB 11; Length 309; Best Local Similarity 98.4%; Pred. No. 2.2e-119; Matches 304; Conservative 4; Mismatches 1; Indels 0;
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                                                                                                                          309 AA; 35623 MW; 9162487561CF44E7 CRC64;
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Last annotation update)
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InterPro; IPR001245; Tyr_pkinase.
Pfam: PF000169; Pkinase; 1.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
SCATING/threonine-protein kinase.
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001249; Sex_thr_pkinase.
InterPro; IPR001249; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; STRC; 1.
SMART; SM00219; TyrEC; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 357 AA; 40189 WW; IFA184EEFA9;
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EMBL; AF286366; AAG00534.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CamKI-like protein kinase.
Homo sapiens (Human).
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                                                                                                                          SEQUENCE
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                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                    1 MGRKEEDDCSSWKKQTINIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPA
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; Pred. No. 3.5e-83;
43; Mismatches 51; Indels 3;
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     Length 357;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
51milar to calloium/calmodulin-dependent protein kinase I.
                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37889CDA717D3AB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probom; PP00069; pkinase; 1.
Probom; PD000001; Euk_pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PS00110; PROTEIN_KINASE_DOM; 1.
PROSITE; PS001108; PROTEIN_KINASE_ST; UNKNOWN_1.
ATP-binding; Kinase; Transferase.
SEQUENCE 374 AA; 41624 MW; 37889CDA717D3AB2
Score 1246; DB 4;
Pred. No. 2.3e-90;
                             ; Pred. No. 2.3e
40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC014825; AAH14825.1; -.
MGD; MGI:2141437; AI505105.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
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                                                                                                              72 LKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 KYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 AQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAA 311
129 VKYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPE 188
                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegious (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Naito Y., Watanabe Y., Yokokura H., Sugita R., Nishio M., Hidaka H.; "Isoform-specific activation and structure diversity of calmodulin kinase I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 KKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIAV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 343 AA; 38438 MW; 994D451D809A9D80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 VLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 272:32704-32708(1997).

J. Biol. Chem. 272:32704-32708(1997).

I. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

EMBL; BA004267; BAA2863.1; -

HSSP; 063450; 1A06.

InterPro; IPR000719; Euk_pkinase.

InterPro; IPR000719; Euk_pkinase.

ProDom; P0000001; Euk_pkinase; 1.

ProDom; P0000001; Euk_pkinase; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_ADP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ADP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.6%; Score 1070; DB 11; Length 343; 59.5%; Pred. No. 1.8e-76; ive 55; Mismatches 74; Indels 12.
                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) ca2+/calmodulin-dependent protein kinase I beta 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74;
                                                                                                                                                                                                                                                                          343 AA.
                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98070455; PubMed=9405489;
                                                                                                                                                                            | ||| |||||||||| : | | ATAVVRHMRKLQLGTSQEG 327
                                                                                                                                                          310 AAAVVHHMRKLHMNLHSPG 328
                                                                                                                                                                                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Sim
Matches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                          070150
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 AQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 DFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 KKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIAV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 EQKPYGKAVDVWALGVISYILLCGYPPFYDESDPELFSQILRASYEFDSPFWDDISESAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yokokura H., Terada O., Naito Y., Hidaka H.;
"Isolation and comparison of rat conwas encoding Ca2+/calmodulin-
dependent protein kinase I isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.5%; Score 1068; DB 11; Length 342; 60.1%; Pred. No. 2.6e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodom; Profoso; Prinase; 1.
Prodom; Profoso; Euk_pkinase; 1.
Prodom; Profoso; Euk_pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS01011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS0108; PROTEIN_KINASE_ST; 1.
ATP-binding; Serine-threonine-protein kinase; Transferase.
SEQUENCE 342 AA, 38463 WW; 546C464913E784A2 CRC64;
312 AVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAP 359
                                   SFLRHIRKL-----GOSPEGE----EASROGMTRHSHPGLGTSQSP 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53; Mismatches
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                                                                                                                                                                                                                                                      Created)
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01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97228532; PubMed=9074610;
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                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 01-JUL-1997 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel. Protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IISSUE=BRAIN
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                                                                                                                                         RESULT 9
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132 KYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVL 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLOIQKNFAKSKWRQAFNAA 311
                                                                                                                                                                                                                                  MEDLINE=97432815; PubMed-9286695; Brenner V., Nyakatura G., Rosenthal A., Platzer M.; Gronganization of two novel genes on human Xq28: compact head to head arrangement of IDH gamma and TRAP delta is conserved in rat and mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 KKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIAV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 EQXPYGKAVDVWALGVISYILLCGYPPFYDESDPELFSQILRASYEFDSPFWDDISESAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 LKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 343 AA; 38500 MW; E954AEE89DE608C9 CRC64;
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Ca2+/calmodulin-dependent protein kinase I.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.7%; Score 1047; DB 4;
60.7%; Pred. No. 1.2e-74;
Live 52; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pfam; PF00069; pkinase; 1.
PrNTAS; PR00109; TYRKINASE.
Probom; PD00001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 AVVHHMRKLHMNLHSPGVRPEVENRPPETQA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFLRHIRKL -----GQIPEGEGASEQGMA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U52111; AAF74509.1; -. HSSP; Q63450; 1A06.
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Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                           Genomics 44:8-14(1997).
                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                          Platzer M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                    CAMKI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 KYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVL 191
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                       MEDLINE-20139438; PubMed=10673339;
MEDLINE-20139438; PubMed=10673339;
Gardner H.P., Rajan J.V., Ha S.I., Copeland N.G., Gilbert D.J.,
Caparkins N.A., Marquis S.T., Chodosh L.A.,
"Cloning, Characterization, and Chromosomal Localization of Pnck,
Ca2+/Calmodulin-Dependent Protein Kinase.";
Genomics 63:279-288(2000).
-! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL, AB023027; BAAR7926.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0109; TYRKINASE.
PRODOM; PRO01001; EUK_pkinase; 1.
PROSTIE; PS00107; PROTEIN KINASE_ATP; 1.
PROSTIE; PS0011; PROTEIN_KINASE_DOM; 1.
PROSTIE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSTIE; PS00108; PROTEIN_KINASE_TF; 1.
ATP-binding; Serine(*Heronine-protein kinase; Transferase. SEQUENCE 343 AA; 38519 WW; 1B4A28B336E7A936E CRC64;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MCAMK1-BETA2 protein (Pregnancy upregulated NONUBIQUITOUS
CA2+/calmodulin-dependent kinase PNCK).
PNCK OR CAMKIB OR MCAMK1-BETA2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                   SEQUENCE FROM N.A.
Ueda I., Minami Y.;
"mCaMK1-beta2.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.3%; Score 1064; DB 11;
59.2%; Pred. No. 5.4e-76;
iive 55; Mismatches 75;
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MGD; MG1:1347357; Pnck.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001299; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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Best Local Similarity 59.2°
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00069; pkinase;
                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                              TISSUE-BRAIN;
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ID Q9NNY2
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Length 343; Indels

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PRELIMINARY;
PRELIMINARY;
                                                                       Caenorhabditis elegans.
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                   01-MAY-2000 (
01-MAY-2000 (
01-MAR-2002 (
                                                                                                                                                          Eto K., Takal
Tokumitsu H.
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Q9V3I4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                       Pfam; PF00069; pklnase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; UNKNOWN_1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS01008; PROTEIN_KINASE_ST; 1.
ATP-binding; Hypothetical protein; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                           Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AF099924; AAF23187.1; -.
HSSP; Q63450; 1A06.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR0002390; Ser_thr_pkinase.
Pfan. PF00069.
                                                                                                                    investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                                                                                                                              STRAIN=BRISTOL N2;
Davidson S., O'Neal D.;
"The sequence of C. elegans cosmid K07A9 ";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                           348 AA; 39124 MW; 88525C390BOA709F CRC64;
Last annotation update)
                                                                                            STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: | :: :| :: : | LOMLRLSSNSNRLQKQASQQQPE 340
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           Hypothetical 39.1 kDa protein.
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 185; Conservative
                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                       Waterston R.; "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                  SEQUENCE FROM N.A.
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Tackumizeru H.;

"Ca2+/calmodulin-dependent protein kinase cascade in Caenorhabditis
elegans. Implication in transcriptional activation.";
L. Shol. Chem. 274:22556-22562(1999).

"I. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

EMBL; AB021864; BAA82674.1;
"InterPro.; IPR002299; Ser_thr_pkinase.

InterPro.; IPR002299; Ser_thr_pkinase.

R InterPro; IPR002299; Ser_thr_pkinase.

R Probom; PD000001; Buk_pkinase; 1.

R SMART: SMO0201; Euk_pkinase; 1.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

R PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00109; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00109; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00109; R PROTEIN_KINASE_ST; 1.

R ATP-binding; Kinase; Serine/Khreonine-Protein kinase; Transferase.
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                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda, Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STAIN-BRISTOL N.2.
MEDLINE-99357789; PubMed-10428833;
ELO K., Takahashi N., Kimura Y., Masuho Y., Arai K., Muramatsu M.,
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Last annotation update)
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Last annotation update)
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348 AA.
                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence u 01-MAR-2002 (TrEMBLrel. 20, Last annotation ca2+/calmodulin-dependent protein kinase I. CMK-1.
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                                                (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 20,
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Matches 185; Conservative (
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RESTRAINEBRENELY, ALLY, RAY, BOLLER, A., GOCAYDE J.D., RA Adams, M.D., Celniker S.E., Iti P.W., Hoskins R.A., Galle R.F., Andanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Gacrge R.A., Lewis S.E., Richards S., Ashburnar M., Henderson S.N., RA Ganner G.C., Wortman J.R., Yandell M.D., Zhampe M., Pfelifer B.D., Randon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfelifer B.D., RA Ballew M., Daybani A., An H.J., Andrews-Feankoch C., Baldwin D., Ballew M., Pallew R.M., Basul A., Barchale J., Baryaktaraju L., Basaley E.M., Rallew R.M., Basul A., Barchale J., Barckstein P., Bortler P., Chandra I., Randella M., Burtis C., Barawa D.A., Daller H., Cadieu E. Center A., Chandra R. Besson K.Y., Danker B. Delcher A., Dalle C., Dewenport L.B., Davis S., Chandra I., Charley S., Danke C., Davis C., Perrara C., Perrara S., Pleischmann W., Roughlos B., Delcher A., Dang Z., Walsy A.D., Dew I., Datez S., Dunn P., Douris M., Jougan Rocha S., Dunkov B.C., Dunn P., Douris M., Jougan R., Jouris M., Jougan R., Statis M., Mandel B.E., Kodira C., Perrara C., Ferrara S., Rull Db., Lai Z., Lang Y., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPharm C., McLeod M.P., McRaft C., Ravitz S., Rull Db., Lai Z., Lang Y., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPharmson D., McHand B.C., Stander K., Saunders R.D.C., Scheeler F., Shen H., Rallazolo M., Pittman G.S., Bunner S., Pollard J., Pull Z., Lang Y., Massarman D. R., Mandels R., Wassarman D. R., Weinsenbach J., Rallazolo M., Pittman G.S., Sunders R.D.C., Scheeler F., Shen H., Wang Z.-Y., Wassarman D. D., Weinser D. W., Weinsenbach J., Wang Z.-Y., Wassarman D. D., Weinser D. W., Weinsenbach J., Rull G., Schole L., Sunder R., Weinser B., Weinsen D. Stong S., Zhan M., Zhang S., Zhao W., Zhan W., Zhang S., Zhao W., Zhao S., Zhao W., Zhang S., Zhao S., Zhao W., Zhao S., Zhao W
                     Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                             Xu X.Z.S., Wes P.D., Chen H., Li H.S., Yu M., Morgan S., Liu Y.,
                                                                                                                                                                                               "Retinal targets for calmodulin include proteins implicated in synaptic transmission."; J. Biol. Chem. 273:31297-31297(1998).
  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE; PSO011; PROTEIN_KINASE_DOM; 1.
PROSITE; PSO0108; PROTEIN_KINASE_ST; 1.
ATP-binding; Alternative splicing; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD000001; Euk_pkinase; 1.
SM00220; S_TKC; 1.
                                                                                                                          TISSUE-RETINA;
MEDLINE-99030403; PubMed-9813038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AE003844; AAF59343.1; -. EMBL, AE003844; AAF59344.1; -. HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00069; pkinase;
                                                                                                       SEQUENCE FROM N.A.
                                            Ephydroidea; Dros
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                          STRAIN-BERKELEY;
                                                                                                                                                                                    Montell C.;
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PENLLYYSPDDDSKIMISDF -> VRQFYLIYIFNDHLALR
KIGK (IN SHORT ISOPORM).
MISSING (IN SHORT ISOPORM).
BDE60C6C981CFBC4 CRC64;
                                                                                                                                                                                              ELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMIT 163
                                                                                                                                                                                                                                                                                      164 DFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEET 223
                                                                                                                                                                                                                                                                                                                                          224 ESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTAL 283
                                                                                                                                                                                                                                                                                                                                                          249 DANLFAQILKGDFEFDSPYMDEISESAKHFIKNLMCVTVEKRYTCKQALGHAWISGNEAS 308
                                                                                                                                                                             59 AFRDSSLENEIAVLK-------KIKHENIVTLEDIYESTTHYYLVMQLVSGG 103
                                                                ; Score 957.5; DB 5; Length 405;
; Pred. No. 1.8e-67;
64; Mismatches 70; Indels 19; Gaps
                                                                                                                                       2 GRK-EEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQR-LTGKLFALKCI-KKSP 58
                                                                                                                                                                                                                                                                                                   Score 747.5; DB 4; Length 501; Pred. No. 9.4e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019356; AAH19256.1;
EMBL; BC017363; AAH17363.1;
InterPro; IPR000104; Antifreeze_1.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 protein.
501 AA; 54353 MW; 1D6DBF8ABA0D1D70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              284 HRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNLHS 326
                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 54 4 kba protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           501 AA
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PRINTS; PR00308; ANTIFREEZEI.
ProDom; PD000001; Euk_pkinase; 1.
                                           45113 MW;
                                                                   38.1%;
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35.9%;
                                                                                    Best Local Similarity 55.4*
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                          405 AA;
                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                              191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                              VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                      Query Match
    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSWTT8;
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Search completed: March 14, 2003, 14:09:39 Job time: 35 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2234 GICCTCCGIGCACACACCAAIGGAGITAACCIIGGAAGIIGACIAITITAAIGICIGCC 2293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2294 AGGAGTTCTAATCCTGCCTCTGTTCCCTTTTCTCTTGAAAGTCCAGCACACCATTCT 2353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2354 TGTCCTTCCCCAGITTCCTCGCCCTCCAGCTTCAGCTTCAGGGTTGTGCT-T 2412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2174 AAGTGGAATAGAAAGAAGTTCATGAGTAAGGGCTGCAAGGAATTCTTATCCTGGCCACAT 2233
                                                                                                                                                                                                                                                                                        TGGCCAGGCTGTGTCACCTTCTCCAAGCAAAGCCATATGGAGCATCTACCCAGACTCCCA 1934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1943 CTCTGCAGACTCGCTCCTGCCTATCT------GGCCTCACGGCCAGACTGGACCCAT 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2055 TGAGCTCTTCAAGTTCTAATCCTTAACTCCAGGATTAGCTCCCAAGTGCGCTGAGACCCA 2114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1487 GGTGGGCAGACTGGGGTGTGTCTCGTTATGTGATCCCAGGAGCCCATGTGGTTTTCAGGA 1546
                             CAATTITCAGGAGACATATTCAACTCCTCTGCTCTTCCAAACCTGGTGTCTATCCGGCAG 1587
                                                                                                                                                                      1708 AGAAGCCTTGTTGAAGCTGTGAGCAGGAGAAGCGGT-------GCCCACCAGCT 1754
                                                                                                                                                                                                                                          AGTGTACGTAGATAGCTCTCGCCTGGGTCTGTGCTGTTTGTCGTGAAAAGCTTAATGGGC 1874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1995 TAATGTCGTTGCCTGCCCATCTGCATGAATGACAGGCAGCTCCCCATGGTGGTGTCTGCCTG 2054
                                                                                                                                                                                                                                                                                                                                                      2219 ACCTCATATTACCCTAATTAAGG-----ATTCGGGGACTATTTCCATGTCATCC
                                                          1547 GACATTCCTG--GCTCTTCTCTGCTCTGAGCTGGCATCTGCCCTGAGGAAGGGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTGCACACACTCCCACCTCTCAAGCCTCCAACCTCTTGGCCCAGATTGGGCTCAT
                                                                                       1588 AGGCAGGAAGGCAGAGCAAGTGGAGCAGGGCTTAGCAGGAGCAGTTTCTGGCCAGAAGCA
                                                                                                                                                    1755 rccaggrerccrgacergererargececacaceracergegegegetergrge
                                                                                                           AATAAAATGGACATATTTTTCTCTAAAAAAAAAA 2447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATAAAAATGGACATATTTTCTCTAAAAAAAAAA 2411
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HS272L16 by DNA linear PRI 23-NOV-1999 Undan DNA sequence from clone 272L16 on chromosome 1422.1-32.3. Contains the 3' end of the LAMB3 gene for Laminin, Beta 3 (Nicein, Ralinin, BM600) and a novel Rat Ca2+/Calmodulin dependent Protein

LOCUS DEFINITION

RESULT 8 HS272L16

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272L16 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://Dacpac.med.buffalo.edu/ VECTOR: pCYPAC2 This sequence was generated from a human chromosome 1 bacterial clone contig constructed in collaboration by the Sanger Centre chromosome 1 mapping group and Brian Schutte, Bryan Bjork, Kevin Coppage and Jeffrey Murray. Department of Pediatrics, University of Iowa, USA. Further information can be found at
                                                                                                                                                                                                                                                                                                                             Submitted (27-NOV-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
on Dec 12, 1998 this sequence version replaced gi:3873472.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              only a small overlap as described above.

Hals sequence is the entire insert of clone 272L16. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
          genomic marker D1S491
                                                                                                                                                                                                             Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5972. .6019
/note="MLT1A1 repeat: matches 318. .365 of consensus"
                                                                                                          HTG; BM600; ca repeat polymorphism; Ca2+/Calmodulin dependent
Protein Kinase; D1S491; Kalinin; LAMB3; Laminin Beta 3; Nicein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  consensus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1089. .5338
'note="MLT1A2-internal repeat: matches 358. .1643 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  966. .1078
/note="Mill repeat: matches 281. .410 of consensus"
1082. .1506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1082. 1506
Acte-WarD repeat: matches 1. .426 of consensus"
1585. .1875
Anote-"MLTIAl repeat: matches 1. .319 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .203 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             matches 6. .543 of consensus"
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/note="LTR7 repeat: matches 1. .450 of consensus"
                                                                                                                                                                                                             Craniata; Vertebrata; E
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .302 of
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/hote="MLT1A1-internal repeat: matches 5.
and a ca repeat polymorphism, complete sequence. AL023754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches 101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1898. .2024
/note="MLT11 repeat: matches 58.
2347. .2925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/HGP/Chrl.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     // 2925
/note="MER34 repeat:
3090. 3417
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 157875)
Grafham, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="q32.1-32.3"
/clone="RP1-272L16"
/clone_lib="RPCI-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5339. .5532
                                                                                     AL023754.1 GI:4007152
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                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                Homo sapiens.
Homo sapiens
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                                                                                                                                                                                        ORGANISM
                                                                ACCESSION
VERSION
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                                                                                                                                                                                                                                                                   REFERENCE
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29501...29820.

7004c="MLM11 repeat: matches 141...355 of consensus"
29501...29820.

7004c="MLM11 repeat: matches 1...365 of consensus"
7004c="MLM11 repeat: matches 1...365 of consensus"
7004c="MLM11 repeat: matches 355...618 of consensus"
70095...30028

7004c="HAM11 repeat: matches 683...874 of consensus"
7004c="HAM11 repeat: matches 683...874 of consensus"
7004c="HAM11 repeat: matches 1189...1455 of consensus"
7004c="Cham11ela repeat: matches 11.306 of consensus"
7004c="Cham11ela repeat: matches 11.25...1189 of consensus"
7004c="Cham11ela repeat: matches 11.25...1189 of consensus"
7100...31107
71100...311107
711101...31211
7004c="LLM44 repeat: matches 5448...6190 of consensus"
71923...32141
7004c="LLM2 repeat: matches 5...426 of consensus"
71925...33436
7004c="LLM2 repeat: matches 3451...4317 of consensus"
7004c="MLM2 repeat: matches 1...309 of consensus"
7004c="MLM2 repeat: matches 1...309 of consensus"
7004c="MLM2 repeat: matches 761...3451 of consensus" ö OY 1690 GAGGGAGCCCCAAGGCGTAGAAGCCTTGTTGAAGCTGTGAGCAGGAGAAGCGGTGCCCAC 1749
Db 147651 GAGGGAGCCCCAAGGCGTAGAAGCCTTGTTGTAGTGAGCGAGGAGAAGCGGTGCCCAC 147710 DD 147591 AGTITCTGGCCAGAAGCACCAGCCTGCTGCCAGCGGGGCAGCCCCTCATAGGAGGCCCAG 147650 70817. 38850 7004="Charliela repeat: matches 1. .1142 of consensus" 3923. 39437 7004="MIR repeat: matches 1. .140 of consensus" complement(39554. 39839) 7004="Match: GSS AQ070531" 7105="match: GSS AQ070531" 7105="Lepeat: matches 2180. .2489 of consensus" 41615. .41810 QY 1570 CTGGTGTCTATCCGGCAGAGGAAGGCAGAGCAAGTGGAGCAGGGCTTAGCAGGAGC 1629 AGTITCIGGCCAGAAGCACCAGCCTGCTGCCAGCGGGGCAGCCCCTCATAGGAGGCCCAG 1689 CAGCTTCCAGGTCTCCCTGACCTGCTCTATGCCCCACCCTACGTGCCGTGCGTC 1809 1510 CCTGTGCCTATGTCACTGCAATTTTCAGGAGACATATTCAACTCCTCTGCTCTTCCAAAC 1569 /note="L2 repeat: matches 2292. .2723 of consensus" 27779. .27820 /note="10 copies 4 mer caca 100% conserved" 29036. 29195 //note="HALL repeat: matches 4. .163 of consensus" 29263. 29500 Length 157875; ., // conserved mer ca 100% conserved 27779. .27818 Indels .541 of tch 37.0%; Score 905.6; DB 9; al Similarity 98.5%; Pred. No. 4.4e-239; 914; Conservative 0; Mismatches 14; 68. 27357 repeat_region misc_feature Query Match Best Loca Matches 1630 1750 Db 147471 δ

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/traislation="MorkebedcsswkkQttnirktfifmevlgsgafsevflukQrv
TGKLFALKCIKKSPARPDSSLENEIAVLKRIKHENIVTLEDIYESTHYYLVWQLVSG
GELFDRILEBOLYTEKDASLVIQQVLSAVKYLHENGIVHRDKFENLLYTPEBDKKI
MIDDFGLSKMEQUMYWSTAGCTPGYVAPEVLAQKPYSKAVDCMSIGVITYILLGYPP
FYEETESKLFEKIKEGYYFEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALRHPW
                                                                                                                                               87. .>1013
/note="similar to calcium/calmodulin-dependent protein
kinase I mRNA (L24907, L26288)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACTGCAGTTCCTGGAAGAACAGACCACCAACATCCGGAAAACCTTCATTTTATGGAA 150
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                                                                                                                                                                                                                                                                                                                                                                      IDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFN"
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 813; DB 10;
Pred. No. 1.1e-213;
0; Mismatches 95;
                     /organism="Rattus norvegicus"
/db_xref="taxon:10116"
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                                                                     /tissue_type="brain"
/clone_lib="S. Nakanishi"
/dev_stage="embryo (E18)"
                                                                                                                                                                                                                         /product="Protein Kinase"
/protein_id="BAA19880.1"
/db_xref="G1:2077934"
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Best Local Similarity 90.2%;
Matches 870; Conservative
                                                       /clone="N5"
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Submitted (15-JUL-1996) Hisayuki Yokokura, Nagoya University School
of Medicine, Department of Pharmacology; Teurumai 65, Showa-ku,
Nagoya, Aichi G. Japan (Tel:052-744-2075, Fax:052-744-2083)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROD 07-FEB-1999
                                                                                                                                                                                                                                                                                                                              D 147831 TGGGCTGGCCAGGCTGTGTGCCTTCTCCAAGCAAAGCCATATGGAGCATCTACCCAGAC 147890
                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae;
CAGCTICCAGGICICCCIGACCIGCCIGCICIAIGCCCCACACCCIACGIGCCGIGGCIC 147770
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                                                                                                                                                                                 TCCCACTCTGCACACACTCCCCACCTCTCAAGCCTCCAACCTCTTGGCCAGATTGGG 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus embryo (E18) brain cDNA to mRNA, clone_lib:S Nakanishi clone:N5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACATGTCCTCCGTGCACACCCAATGGAGTTAACCTTGGAAGTTGACTATTTTAATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2290 TGCCAGGAGTICTAATCCTGCCTCTGTTCCCTTTGTCTCTTGAAAGTCCAGCACACA
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                                                                                                                                                                                                                                                           CTCATTAATGTCGTTGCCTGCCCATCTGCATGAATGACAGGCAGCTCCCCATGGTGGTGGTCT
                                 TGTGCAGTGTACGTAGATAGCTCTCGCCTGGGTCTGTGCTGTTTGTCGTGAAAAGCTTAA
                                                                                                                                                                                                                                                                                                                                                                                                        2110 ACCCAGCCAGCACTTCTGGCCCTTCTCCCTGCCTCAATCTAAAAGCAGTGCCACACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yokokura, H., Terada, O., Naito, Y. and Hidaka, H. Isolation and comparison of rat cDNAs encoding cat-/calmodulin-dependent protein Kinase I isoforms Biochim. Biophys. Acta 1338 (1), 8-12 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus mRNA for Protein Kinase, partial D86557 101:2077933
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KEYWORDS SOURCE

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ORGANISM

MEDLINE REFERENCE AUTHORS

JOURNAL

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AUTHORS TITLE

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                                                                                                                                                                                                                                                                               53 CTTCAACTCTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAAC 112
                                                                                                           113 AGACCACCAACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCT
                                                                                                                                                                                                                                                                                              ACACAGAGAAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533 AAGAGAACTCTAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGGCA
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0
                                  Length 1738;
                                                             2; Indels
                                  DB 9;
                                  Score 1734.8;
Pred. No. 0;
                                                               0; Mismatches
                                 70.9%;
99.9%;
                                 Query Match 70.9
Best Local Similarity 99.9
Matches 1736; Conservative
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Vkorligklealkotikkspaprdssleneiavlkkirhenivtlediyesthyylvu
Olvsggelfprileroyterdsslivloovlsswyktheneityhrddlebenlivttpe
Enskimitdfelskwednginstactpeyvapevlaokpysskavdowsigyityill
CGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLERDPNERYTCEKA
LSHPWIDGNTALHRDIYPSYSLOIOKNFAKSKWROAFNAAAVHHMKKLHMNLHSPGY
RPEVENRPETGASETSRPSSPEITITEAPVLDHSVALPALTQLPCQHGRRPTAPGGR
SLNCLVNGSLHISSSLYPWHGOSLAAGPCGCSSCLNIGSKGKSSYCSEPTLIKKANK
KONFKSEVMVPVKASGSSHCRAGOTGVCIM"
                                                                                                                                                                                                                                                  at
    PRI 21-APR-1999
Similar to
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1738)
                                                                                                                                                                              Submitssion Submission Submitted (21-APR-1999) E-mail contact: humquery@sanger.ac.uk This sequence was generated from EDNA clones isolated using sequence from the bacterial clone 272116 (ALO23754) and EST data. The EST sequences listed match this sequence with an identity of least 95% between the coordinates shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST AI215131 from clone IMAGE:1925595"
                                                                                                                                                                                                                                                                        Further information can be found at http://www.sanger.ac.uk/HGP/Chr1/ Partial, experimentally determined gene.
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/note="matches EST R05661 from clone 29500"
1484. .1736
HS272L161 1738 bp mRNA linear Human gene isolated from PAC 272L16, chromosome 1, calcium/calmodulin dependent protein kinases.
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/note="matches EST AA351937"
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Location/Qualifiers
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/chromosome="1"
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/note="matches E
764. .843
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Submitted (18-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; I
1 (bases 1 to 2416)
Strausberg,R.
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BC021840. GI:18256866
MGC.
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Bmall: cgapbs refmail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                                                          Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                        Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/Link at: http://image.llnl.gov Series: IRAK Plate: 41 Row: I.Column: 13 Series: IRAK Plate: 41 Row: I.Column: 13 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
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DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
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/clone_lib="NIH_MGC_94"
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Pred. No. 0;
0; Mismatches 494; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pCMV-SPORT6"
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Best Local Similarity 76.1%;
Matches 1853; Conservative (
                                                                Center code: BCM-HGSC
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HS272L161 HS272L161 HWAN gene isolated from PAC 27L16, chromosome 1, similar to calcium/calmodulin dependent protein kinases. ACCESSION AL049688.1 G1:4678721 KEYWORDS SOURCE HOMO sapiens ORGANISM REFERENCE HOMO sapiens ORGANISM FIGURATION REFERENCE HOMO Sapiens ORGANISM FIGURATION REFERENCE AUTHORS AUTHORS TITLE JUDICAT SUbmission JUDICAT SUbmission Sequence from the bacterial clone 272L16 (AL023754) and EST data. This sequences listed match this sequence with an identity of at least 95% between the coordinates shown FEATURES THEP://www.sanger.ac.uk/HGP/Chrl/Partlal, experimentally determined gene. Sanger Centre name: d3272L16.Cll.1. FEATURES Location/Qualifiers Source 1. 1738	Human gene isolated from PAC 272L16, chromosome 1, similar to calcium/calmodulin dependent protein kinases. AL049688 I G1:4678721 AL049688.1 G1:4678721 Homo sapiens. Manmalia: Entheria; Primates; Catarrhini; Hominidae; Homo. Direct Submission Submitted (21-APR-1999) E-mail contact: humquery@sanger.ac.uk This sequence was generated from cDNA clones isolated using sequence from the bacterial clone 272L16 (AL023754) and EST data.	ORIGIN Alignment Scores: Pred. No.: Score: Percent Similarity	432 a es: rity:
Φ	contact: humquery@sanger.ac.uk m. CDNA.clones isolated using e.272116 (ALO23754) and EST data.	Alignment Scor Pred. No.: Score: Percent Simila	es: rity: nlarity:
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rce	1/ Partial, experimentally	Qy 41 Lys	LysGlnArqLeuT
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/organism="Homo sapiens"	"SI	Qy 61 Arg	ArgAspSerSerL
/db_xret="taxon:9606" /chronosome="1"		198	CGGGACAGCAGCC
/map="1432.1-32.3" <11448		Qy 81 Val	ValThrLeuGluA
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/protein_id="cAB41259.1" /db xref="GI:4678722"	1,	101	Sercivelyclut
/translation="STLEAMGRKE VKORIMGKIRDIKCIKKSDEFDRG	KKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFL	1 0	
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LSHPWIDGNTALHRDIYPSVSLQI RPEVENRPPETQASETSRPSSPEI	AQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNLHSPGV PEITITEAPVLDHSVALPALTQLPCQHGRRPTAPGGR	Db 378 AGT	AGTCTGGTGATCC
SLNCLVNGSLHISSSLVPMHQGSL KQNFKSEVMVPVKASGSSHCRAGQ	SSLAAGPCGCCSSCLNIGSKGKSSYCSEPTILKKANK AGQTGVCLIM"	Oy 141 His/	HisArgAspLeuI
exon <1107 //number=1		Db 438 CAC	CACAGAGACTTA
exon 108. 236		Oy 161 Met	MetileThrAspF
exon 231		Db 498 ATG	ATGATCACTGACT
exon 312 450		Oy 181 Gly	GlyThrProGlyT
451574		111 DP 558 GG	GGGACCCCAGGCT
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/number=6 exon 651763		 Db 618 GAT	GATTGCTGGTCCA
nisc_feature 653.777	/number=/ 653777	Oy 221 Glu	GlugluThrGlus
/note="matches EST AI215 exon 764842	215131 from clone IMAGE:1925595"	 Db 678 GAA	GAAGAAACGGAGI
/number=8 exon 843.,930		Qy 241 Pro	ProPheTrpAspA
/number=9 misc_feature 868.,1159		738	CCATTCTGGGATC
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                                                                                                                                                           GGTGCCCACCAGCTTCCAGGTCTCCCTGACCTGCTGCTCTATGCCCCACACCCTACGTG
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                                       CCGTGGCTCTGTGCAGTGTACGTAGATAGCTCTCGCCTGGGTCTGTGTTTTGTCGTGA
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                              GAGGCCCAGGAGGCCCCCAAGGCGTAGAAGCCTTGTTGAAGCTGTGAGCAGGAGAAGC
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Antinitor's disease, amyotrophic utilisation of the activities such as: Immune system suppression, Activinibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
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Zhang J;
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Best Local Similarity 99.5%; Pred. No. 0;
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Wehrman T,
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Wang Z,.
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

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                                       March 14, 2003, 17:36:01; Search time 328 Seconds
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nucleic search, using frame_plus_p2n model
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2513
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Command line parameters:
-MODEL-frame+p2n.model -DEV=Xlh
-MODEL-frame+p2n.model -DEV=Xlh
-Q-/cgn2_1/USPTO_spool/US09960643/runat_07032003_090517_19867/app_query.fasta_1.647
-Q-/cgn2_1/USPTO_spool/US09960643/runat_07032003_090517_19867/app_query.fasta_1.647
-DB-N_Geneseq_101002 -QFMT-fastap -GUFFIX-p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT-0 -UNITS-bits -START-1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN=15
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXIEN-200000000
-USER-USO960643_GCGN_1_1_263_grunat_07032003_090517_19867 -NCPU=6 -ICPU=3
-NOLXDXY -NOLMMAP -LARGEQDERY -NEG_SCORES-0 -WAIT -LONGIGG -DEV_TIMEOUT-120
-WARN IIMEOUT-30 -THREADS-1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

N_Geneseq_101002:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

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ALIGNMENTS

AAI60703 standard; cDNA; 1956 BP (first entry) 22-OCT-2001 AAI60703; RESULT 1

Human polynucleotide SEQ ID NO 4692

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia; ss.

Homo sapiens

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CGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCATGAAAACATT

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM8642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system disease, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic activity, chemoteactic/chemokinetic activity, haemostatic as infune system suppression, and thrombolytic activity, chemoteactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and c.N.S disorders.
                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                            Wang
                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang
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Yang Y,
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                                                                                                    2000US-0488725.
2000US-052317.
2000US-0598042.
2000US-0653450.
2000US-0653450.
2000US-0633036.
2000US-0633036.
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09-JUL-2000;
19-JUL-2000;
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29-NOV-2000;
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                                           26-JUL-2001
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Wang J, ¥
Zhao QA,
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Alignment Scores:

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Length: 1956

Scorer

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LysGlnArgLeuThrGlyLysLeuPheAlaLeuLysCyslleLysLysSerProAlaPhe

1144 1084 340 360 400 220 240 260 280 320 100 364 120 424 140 484 160 544 180 604 200 664 724 784 844 904 300 964 ProThrAlaProGlyGlyArgSerLeuAsnCysLeuValAsnGlySerLeuHis1leSer 1025 CACATGAACCTGCACAGCCCGGGCGTCCGCCCAGAGGTGGAGAACAGGCCGCCTGAAACT 301 LysSerLysTrpArgGlnAlaPheAsnAlaAlaAlaValValHisHisMetArgLysLeu LeuAspHisSerValAlaLeuProAlaLeuThrGlnLeuProCysGlnHisGlyArgArg HisMetasnLeuHisSerProGlyValargProGluValGluAsnArgProGluThr HisargaspLeuLysProGluAsnLeuLeuTyrLeuThrProGluGluAsnSerLysIle GlyThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLysAlaVal AspCysTrpSerIleGlyValIleThrTyrIleLeuLeuCysGlyTyrProProPheTyr 665 GATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCCCCCATTCTAT GluGluThrGluSerLysLeuPheGluLysIleLysGluGlyTyrTyrGluPheGluSer ProPheTrpAspAspIleSerGluSerAlaLysAspPheIleCysHisLeuLeuGluLys 261 AspproAsnGluArgTyrThrCysGluLysalaLeuSerHisProTrpIleAspGlyAsn 845 GATCCGAACGAGCGGTACACCTGTGAGAAGGCCTTGAGTCATCCCTGGATTGACGGAAAC 281 ThralaLeuHisArgAspIleTyrProSerValSerLeuGlnIleGlnLysAsnPheAla 341 GlnAlaSerGluThrSerArgProSerSerProGluIleThrIleThrGluAlaProVal SerCysLeuAsnIleGlySerLysGlyLysSerSerTyrCysSerGluProThrLeuLeu GTGACCCTGGAGGACATCTATGAGAGCACCACCACTACTACCTGGTCATGCAGCTTGTT ValThrLeuGluAspIleTyrGluSerThrThrHisTyrTyrLeuValMetGlnLeuVal SerLeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIleVal 241 321 381 1265 1325 361 401 421 81 305 365 425 141 485 181 605 201 221 101 121 g g g g g Qγ g QΥ g δŽ g QΫ 8 ò В ŏ δy q g δŸ g δy g οy g οy a Óγ òγ δy g QY õ δ g δý

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The invention relates to a method for screening biologically active agent that modulates cancer associated protein kinase function. The invention also relates to a method for diagnosing cancer comprising determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase. The method is useful for diagnosing cancer. A protein kinase is useful for screening biological agents that modulate cancer associated protein kinase function. Downrequlating the activity of protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon cancer. A nucleic acid encoding protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon cancer. A nucleic acid encoding protein kinase is useful to screen biopsy derived tumours and inflammatory samples such as arthritic synovium, for amplified DNA in the cell or increased expression of corresponding mRNA or protein and is also useful to detect differences in expression levels cancer as molecular weight, amino acid and nucleotide sequences between the two cells. The present sequence is human calmodulin kinase CAMK-XI gene
                                                                                                                                                                                                                                                                                     Human; cytostatic; antisense gene therapy; screening; protein kinase;
cancer; liver; colon; tumour; inflammation; arthritic synovium; CAMK-X1;
calmodulin kinase; enzyme; gene; chromosome 1q32.1-32.3; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing cancer, comprises determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase or upregulation of expression of the protein kinase, in the cancer
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                                                                                                                                                                                                                                                      Human calmodulin kinase, CAMK-X1 gene.
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UNIV BRITISH COLUMBIA.
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2000US-237423P.
2000US-238558P.
2001US-290555P.
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P-PSDB; AAE22764.
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02-0CT-2000;
04-0CT-2000;
10-MAY-2001;
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March 14, 2003, 10:03:49; Search time 566 Seconds (without alignments) 9736.113 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseg/genesegn-embl/NA2001A.DAT:*/SIDS2/gcgdata/geneseg/genesegn-embl/NA2001B.DAT:*/SIDS2/gcgdata/geneseg/genesegn-embl/NA2002.DAT:*

/SIDS2/gcgdata/geneseg/genesegn-emb1/NA1999.DAT:*/SIDS2/gcgdata/geneseg/genesegn-emb1/NA2000.DAT:* /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*

Description	Human calmodulin k Human polynucleoti Human polynucleoti Human diagnostic a Human CaM kinase I Human kinase (PKIN Nucleotide sequenc Human polynucleoti
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SUMMARIES	AAD36140 AAI58917 AAS31014 ABL60905 AAD18826 AAH25120 AAI58638
EQ.	22224222 222242222
Length	2447 1956 2165 2689 2689 1565 1661 1733 1733
% Query e Match Length DB	100.0 78.3 75.8 72.0 20.6 20.6 20.6 20.6 20.6
Score	2447 1915 1915 1954.6 504.6 504.6 504.6 504.6 504.6
Result No.	108459C

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ALIGNMENTS

AAD36140 standard; DNA; 2447 BP.

RESULT 1

AAD36140;

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Human; cytostatic; antisense gene therapy; screening; protein kinase; cancer; liver; colon; tumour; inflammation; arthritic synovium; CAMK-X1; calmodulin kinase; enzyme; gene; chromosome 1q32.1-32.3; ds.
                                                                                                                   Location/Qualiflers
70.1500
/*tage /
/product= "Human CAMK-X1 protein"
                                      Human calmodulin kinase, CAMK-X1 gene.
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2000US-237419P.
2000US-237423P.
2000US-238558P.
2001US-290555P.
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                   (first entry)
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02-OCT-2000; 2
02-OCT-2000; 2
04-OCT-2000; 2
10-MAY-2001; 2
                                                                                                  Homo sapiens.
                  09-AUG-2002
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                                                                                                                       Key
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XX (KINE-) KINETEK PHARM INC.

PA (UYBR-) UNIV BRITISH COLUMBIA.

XX YA

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WPI; 2002-394145/42.

DR P-PSDB; AAE22764.

DR P-PSDB; AAE22764.

DR P-PSDB; AAE22764.

PT of a nucleic acid sequence encoding a protein kinase or upregulation of expression of the protein kinase, in the cancer.

TO f a nucleic acid sequence encoding a protein kinase or upregulation of expression of the protein kinase, in the cancer.

XX The invention relates to a method for screening biologically active agent that modulates cancer associated protein kinase function. The invention cancer associated protein kinase function of expression of a nucleic acid sequence encoding a protein kinase. The method is useful for diagnosing cancer. A protein kinase is useful for screening biological agents that modulate cancer associated protein kinase function. Downregulating the acid encoding protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon cancer. A nucleic acid encoding protein kinase is useful to screen biopsy derived tumours and inflammatory samples such as arthritic synovium. For amplified DNA in the call or increased expression of corresponding mRNA corporated and is also useful to detect differences in expression levels cuch as molecular weight, amino acid and nucleotide sequences between the corporated on chromosome 1932.1-32.3.

XX Sequence 2447 BP; 590 A; 707 C; 604 G; 546 T; 0 other;
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Ouery Match

Best Local Similarity 100.0%; Score 2447; DB 24; Length 2447;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2447; Conservative 0; Mismatches 0; Indels 0; Gaps

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                  TGGAGTGGGAGCTCAAGCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAACT
                           CAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAG
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          AGCAGGAGCAGTTTCTGGCCCAGAAGCACCAGCCTGCTGCCAGCGGGGCAGCCCCTCATAG
                                        CCGTGGCTCTGTGCAGTGTACGTAGATAGCTCTCGCCTGGGTCTGTGTTTGTCGTGA
                                                                                                                                CCGTGGCTCTGTGCAGTGTACGTAGATAGCTCTCGCCTGGGTCTGTGTTTGTCGTGA
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                                                                    GGTGCCCACCAGCTTCCAGGTCTCCCTGACCTGCTGCTCTATGCCCCACACCCTACGTG
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                             GAGGCCCAGGAGGCACCCCAAGGCGTAGAAGCCTTGTTGAAGCTGTGAGCAGGAGAAGC
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Human polynucleotide SEQ ID NO 4692.
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The Invention Teatures to numen nucrear actus, containing the encoded polypeptides (AAM38642-AAM4213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, auch as Alzhaimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotexic/chemokinetic activity, haemostatic and thrombolytic activity, chemotexic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and constitutions. The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                      Wang
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tu C, Xue AJ,
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                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                        Wang
                                                                                                                                                      disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACACGCATCCTCAGAAGCTTCAACTCTGGAGGCAATGGGTCGAAAGGAAGAAGATGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCACCACCACTACTACTACTGGTCATGCAGCTTGTTTCTGGTGGGGGAGCTCTTTCACCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 2165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                      treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2165 BP; 533 A; 613 C; 563 G; 455 T; 1 other;
                                                      Qian XB,
Yang Y,
                                                                                                                                                    for
                                                     uc, Mar, Cuc, Xuc AJ, Drmanac RT;
                                                                                                                                                    useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1854.6;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                           NO 1120; 10078pp; English.
                                                                                                                                                    polypeptides, us
system injuries
                                                     Chen R,
Xu C, X
                                                     Asundi V, Che
Wehrman T, Xu
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 75.8%;
Best Local Similarity 98.3%;
Matches 1914; Conservative
29-NOV-2000; 2000US-0727344
                                                                                                                                                 Novel nucleic acids and
                                                                                                                                                                such as central nervous
                                                                                                          2001-442253/47.
                                                     Liu C, A
Wang Z, W
                            HYSEQ INC
                                                                                                                         P-PSDB; AAM39761
                                                                                                                                                                                                                                                                                                                                                                                         assays for recep
C.N.S disorders.
                                                                                                                                                                                           Claim 1; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                specification
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О.
                                                     YT,
                          (HYSE-)
                                                     Tang
Wang
Zhao (
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TCTGGCCAGAAGCACCAGCCTGCTGCCAGCGGGGCAGCCCCTCATAGGAGGCCCAGGAGG 1693
                                                                                                                                                                                                           TTCCAGGTCTCCCTGACCTGCCTGCTCTATGCCCCACACCCTACGT-GCCGTGGCTCTGT 1812
                                                                                                                                                                                                                                      GCAGTGT--ACGTAGATAGCTCTCGCCTGGGTCTGTGCTGTTGTCGTGAAAAGCTTAAT 1870
                                                                                                                                                                                                                                                                                                                                            GGGCTGGCCAGGCTGTGTCACCTTCTCCAAGCCAAATGGAGCATCTACCCAGACT 1930
                                                                                                                                                                                                                                                                                                                                                                                                                                            2078 GGGCTGGCCAGGCTGTCACCTTCTCCAAAGCCAAAAGGAACATCTACCCAGACT 2137
                           1838 TCTGGCCAGAAGCACCAGCCTGCTGCCAGCGGGGAGCCCCTCATAGGAGGCCCAGGAGG 1897
                                                                                                  GAGCCCCAAGGCGTAGAAGCCTTGTTGAAGCTGTGAGCAGGAGAAGCGGTGCCCACCAGC 1753
                                                                                                                                 Human; receptor; diagnostic; therapeutic; gene therapy; vaccine; cell proliferative disorder; Crohn's disease; lymphoma; leukaemia; acquired immune deficiency syndrome; AIDS; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human diagnostic and therapeutic polynucleotide (DITHP) #29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCACTCTGCACACTCACTCCCACCT 1958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2138 CCCACTCTGNACACACTCACCTCCCACCT 2165
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2000US-0184777.
2000US-0184813.
2000US-0184837.
2000US-0184837.
2000US-0184837.
2000US-0185213.
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2000US-0204908.
2000US-0205232.
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2000US-0184698.
2000US-0184768.
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2000US-0184770.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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24 - FEB - 2000;
24 - FEB - 2000;
24 - FEB - 2000;
24 - FEB - 2000;
24 - FEB - 2000;
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24 - FEB - 2000;
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24 - FEB - 2000;
24 - FEB - 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-FEB-2000;
24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6-MAY-2000
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1634
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AAS31014
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The invention relates to polynucleotides (I) encoding diagnostic and therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, conditionally provided in growth and development and receptors. (I) and and proteins involved in growth and development and receptors. (I) and associated with inappropriate DITHP expression. For example, (I) and consider the activity of the DITHPS, by expressing inactive proteins cappelementing the patient's own production of them. (I) and (II) may be used to treat diseases, for example, call proliferative proteins consupplementing the patient's own production of them. (I) and (II) may be used to treat diseases, for example, call proliferative disorder, crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma, continually and culturing the DITHPS, by inscrting the nucleic acids into a host call and culturing the cell to express the protein. (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in camples, and therefore which patients may be in need of restorative capped antibodies and activity. The anti-DITHP actibodies and antibodies may also be used as adiagnostic agents for detecting the capped or produce of DITHPP in samples, or antibodies may also be used as diagnostic agents for detecting the capped or presence of DITHPP in samples, or assay (EILSA), has samples, e.g. by enzyme linked immunosorbant capped to the patient of the patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
                                                                                                                                                                                                                                                                                                            Jones AL;
Daffo A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCCTGGAAGAAACAGACCACCAACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79; Gaps
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                                                                                                                                                                                                                                                        Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC; Chen A, D'Sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE; Dufour GE, Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones Liu TF, Roseberry AM, Rosen BH, Russo FD, Stockdreher TK, Daffo Warlght RJ, Yap PE, Yu Ty, Bradley DL, Bratcher SR, Chen W; Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCATCCTCAGAAGCTTCAACTCTGGAGGCAATGGGTCGAAAGGAAGAAGAAGATGACTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1761.6; DB 22; Length 2689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0;
0; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2689 BP; 642 A; 748 C; 678 G; 621 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapeutic (DITHP) polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 310-311; 522pp; English.
                 17-MAY-2000; 2000US-0204863.
17-MAY-2000; 2000US-020521.
17-MAY-2000; 2000US-0205285.
17-MAY-2000; 2000US-0205286.
17-MAY-2000; 2000US-0205287.
17-MAY-2000; 2000US-020531.
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                                                                                                                                                                                                             (INCY-) INCYTE GENOMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-502867/55.
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Dufour GE,
Liu TF, Rose
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QQ	386	TCTGAAGTGCATCAAGAAGTCACCTGCCTTCCGGGACAGCAGCAGCTGGAATGAGATTGC 445
Qy Db	279	TGTGTTGAAAAAGATCAAGCATGAAAACATTGTGACCCTGGAGGACATCTATGAGAGCAC 338
Qy	339	CACCCACTACTACCTGGTCATGCAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCT 398
Qy	399	GGAGCGGGTGTCTACACAGAGAAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGC 458
Qy Db	459	AGTGAAATACCTACATGAGAATGGCATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCT 518
Qy	519	TTACCTTACCCCTGAAGAGACTCTAAGATCATGACTGACT
Qy Dp	579	GGAACAGAAIGGCAICAIGICCACIGCCIGIGGGACCCCAGGCIACGIGGCICCAGAAGI 638
Qy Dp	639	GCTGGCCCAGAAACCCTACAGCAAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTA 698
Qy	998	CATATTGCTCTGTGGATACCCCCGTTCTATGAAGAACGGAGTCTAAGCTTTTGGAGA 758
Qy Dp	759 926	GATCAAGGAGGCTACTATGAGTTTGAGTCTCCATTCTGGGATGACATTTCTGAGTCAGC 818
Qy Db	819 986	CAAGGACTTTATTTGCCACTTGCTTGAGAAGGATCCGAACGA-GCGGTACACCTGTGAGA 877
Qy Dp	878 1046	AGGCCTTGAGTCATCCCTGGATTGACGGAAACACGGCCTCCACCGGGACATCTACCCAT 937
Qy Db	938	CAGTCA-GCCTCCAGATCCAGAAGAACTTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAAC 996
Qy Dp	997	GCAGCAGCTGTGGT-GCACCACATGAGGAAGCTACACATGAACCTGCACA-GCCCGGGCG 1054
Qy Dp	1055 1226	TCGGCCAGAGGTGGAGAACAGGCCGCGTGAAACTCAAGCCTCAGAACCTCTAGACCCA 1114
QY Db	1115 1286	GCTCCCCTGAGATCACCATCACCGAGGCACCTGTCCTGGACCACAGTGTAGCACTCCCTG 1174
Qy	1175	CCCTGACCCAATTACCCTGCCAGCATGCCGCCGGCCCACTGCCCCTGGTGGCAGGT 1231
Qy	1232	CCCTCAACTGCCTGGTCAATGGCTCCCTCCACATCAGCAGCCTGGTGCCCATGCATC 1291
Qy Db	1292	AGGGGTCCCTGGCCGCCCGGGCCCTGTGCTGCTCC-AGCTGCCTGAACATTGGGAGC 1350

GGCTGGCCAGGCTGTGTCACCTTCTCCAAGCAAAGCCATAT---GGAGCATCTACCC--- 1925 1946 TCTCCCGTGACCTGCCTCTATGCCCCACACCCTACAGTGGCCGTGGCTCTGTGCGAG AAAGGAAAGTCCTCCTACTGCTCTGAGCCCACACTCCTCAAAAAAGGCCAACAAAAAACAG AGGCCAGACTGGAGTCTGTCTCATTATGTGATTCCTGGAGCCTGTGCCTATGTCAC--TG CAATTITCAGGAGACATATTCAACTCCTCTGCTCTTCCAAACCTGGTGTCTATCCGGCAG ACCA----GCCTGCTGCCAGCGGGGCAGCCCTCATAGGAGGCCCAGGAGGAGCCCCAA -GTCTCCCTGACCTGCCTGCTCTATGCCCCACACCCTAC--GTGCCGTGGCTCTGTGCAG TGT--ACGIAGATAGCTCTCG-CCTGGGTCTGTGCTGTTTGTCGTGAAAAGCTTAA--TG -AGACTCCCACTCTGCACACACTCCCACCTCTCTCAAGCCTCCAACCTCTTGGCCAGA TTGGGCTCATTAAT-GTCGTTGCCTGCCCATCTG-CATGAATGACAGGCAGCTCCCCATG GTGGTCTGCCT-GTGAGCTCTTCAAGTTCTAATCCTTAACTCCAGGATTAGCTCCCAAGT 2246 GTGGTCTCCCTGGTGAGCTCTTCAAGTTCTAAATCCTTAACTCCAGGATTAGCTCCCAAGT GCGCTGAGACCCAGCCA - - - GCACACTTCTGGCCCTTCTCCCTGCCTCAATCTAAAAGCA GTGCCACACCCTCCAAA-GTGGAATAGAAAGAAGTTCATGAGTAAG-GGCTGCAAGGAAT TCTTATCCTGGCCA-----CATGTCCTCGTGCACA----CACCCAATGGAGTTA AACTTCAAGTCGGAGGTCATGGTACCAGTTAAAGCCAGTGGCA-GCTCCCACTGCCGGGC Db Db Db Qy Db Oy Oy Oy QΣ QQ Qy Db QQ Dp g Q g δy qq g ŏ g φ DP Qy Ω oy Db ΩŸ Qγ δλ

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----AGTTTCCTCGCCCTCCACCCCTCCAGCTTCATGCTCAGTGTTGTGCTTAATAAAA 2419
         2606 TATGICCTCGGCCCGTCCCGTCCAGGCTTCATGCTCAGAGTTGTGCTTAATAAAA 2665
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptide human CaM kinase I 39.05 and polynucleotide for encoding said polypeptide -
                                                                                                                                                                                      CaM kinase I 39.05; nervous disease; arrhythmia; tumour;
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Pred. No. 4.3e-132;
0; Mismatches 274; Indels
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                                                                                                                                                                  Human Cam kinase I 39.05 polypeptide encoding cDNA
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                                                                                                                                                                                                                                      Location/Qualifiers
18..1085
                                                TGGACATATTTTCTCTAAAAAA 2443
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P-PSDB; ABB08178.
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Human kinase; PKIN; gene therapy; adenocarcinoma; immune disorder; gout; cancer; allergy; sarcoma; leukaemia; acquired immune deficiency syndrome; AIDS; Addison's disease; microbial infection; inflammation; osteoporosis; atherosclerosis; cardiovascular disease; myocardial infarction; anaemia; myasthenia gravis; cirrhosis; cataract; growth and development disorder;
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                                                                                                                                                                                      243 TGCCTTCCGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAAAGATCAAGCATGA
                     194 GAAGGCCAAGGAAAGCAGCATAGAGAATGAGATAGCCGTCCTGAGAAAAAGATTAAGCATGA
                                                                                                        GCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAGAA
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The present invention relates to human kinases (PKIN) and the nucleic acids encoding them. PKIN is used as vaccine and in gene therapy. PKIN is used in the prevention, diagnosis and treatment of diseases cancers, acid in the prevention, diagnosis and treatment of diseases cancers, adenocarcinoma, leukaemia, sarcoma, immune disorder, Addison's disease, acquired immune deficiency syndrome (AIDS), anaemia, asthma, allergies, gout, microbial infections, cardiovascular disease and/or inflammation, myasthenia gravia, atherosclerosis, cirrhosis, osteoporosis, myocardial infarction, cataract, growth and development disorder, seizure disorder, infancation, cataract, growth and development disorder, injud storage infarction, cataract, growth and development disorder, seizure disorder, capumonary embolism, daucher's disease, renal disease and obesity. FKIN may be used to treat disorders associated with decreased PKIN expression by rectifying mutations or deletions in a patient's genome that affect the activity of PKIN by expressing inactive proteins or to cupplement the patients own production of PKIN. PKIN nucleic acids may be used to produce the PKIN polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. PKIN nucleic acid and its complementary sequences may also be used as DNA probes in caid and its complementary sequences may also be used as DNA probes in nucleic acid sequences in samples and therefore which patients may be nown.
seizure disorder; pulmonary embolism; Gaucher's disease; lipid disorder; lipid storage disease; Pick's disease; Tay-Sachs disease; renal disease; obesity; restorative therapy; immunomodulatory; vaccine; cardiovascular; antimicrobial; cytostatic; antiinflammatory; asthma; ss.
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SA, Lu Y;
Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acids, useful for preventing diagnosing and inflammation and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l AR, Tribouley CM, Kearney L, Griffin JA, Nguye, J DAM, Lal P, Burford N, Khan FA, Walia NK, Yao Burrill JD, Marcus GA, Zingler KA, Recipon SA, Phornton M, Tang YT, Hafalla A, Elliott VS, Baug nkumar J, Borowsky ML, Au-young J, Hillman JL;
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                                                                                                                                                                                        /*tag= a
/product= "Human PKIN-11 protein"
                                                                                                                                            Location/Qualifiers
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2000US-200226P.
2000US-202339P.
2000US-203505P.
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Bandman O, Lu DAM, Lal
Patterson C, Burrill JD,
Policky JL, Thornton M,
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Tamkumar J,
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P-PSDB; AAE11777.
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05-MAY-2000;
11-MAY-2000;
18-MAY-2000;
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Walsh RT,
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25-APR-2000;
09-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a kinase polypeptide. The kinase polynucleotides and polypeptides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for the detection of mutant kinases, or inappropriately expressed kinases for the diagnosis of a disease or disorder. They are useful for screening for drugs (or high throughput screening of combinatorial libraries) effective in the treatment of symptomatic or phenotypic manifestations of that disease or disorder. The polynucleotide sequence is useful as a source of probes and primers, which can be used to screen libraries, isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242
                                                                                                                                                                                                                                                                                                                        Novel isolated human kinase polynucleotide that shares structural similarity with animal kinases including calcium/calmodulin-dependent protein kinases, useful in
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                           Nucleotide sequence of a human kinase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 504.6; DB 22;
Pred. No. 4.4e-132;
0; Mismatches 274;
                                                                                                                                                                                                                                                        Friedrich G,
                                                       human disease; human disorder; ss
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                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 32; 32pp; English.
                                                                                                                                                                                                                                                          Turner
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71.3%;
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es 695; Conserv
                                                       Human; kinase;
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                                                                                                                                                                                                 07-DEC-1999;
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 22-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCC
                                                                                                                                                                                                                                                                                                                               720 CCCGTTCTATGAAGAAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGGGCTACTATGA
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                                                                                                                                                                                                     CACTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAG
CATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCTGAAGAGAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polynucleotide SEQ ID NO 841.
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2000US-0552317.
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Human kinase; PKIN; gene therapy; adenocarcinoma; immune disorder; gout; cancer; allergy; sarcoma; leukaemia; acquired immune deficiency syndrome; AIDS; Addison's disease; microbial infection; inflammation; osteoporosis; atherosclerosis; cardiovascular disease; myocardial infarction; anaemia; myasthenia gravis; cirrhosis; cataract; growth and development disorder; seizure disorder; pulmonary embolism; Gaucher's disease; lipid disorder; lipid storage disease; Pick's disease; Tay-Sachs disease; renal disease; asthma; obesity; restorative therapy; cytostatic; immunomodulatory; antimicrobial; cardiovascular; antimiflammatory; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAACTTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGCACACAT 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1051 CGCTGGTGACACACCCCTCAACAAAACATCCACGAGTCCGTCAGCGCCCAGATCCGGAA 1110
                                                                                                                                                                                                                                                                                                          CCCGTTCTATGAAGAAAGGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGGGCTACTATGA
    TAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGG---CATCATGTC
                                                                                            CACTGCCTGTGGGACCCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAG
                                                                                                                                                                                       CAAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Mature human PKIN-2 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and strin, inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and therapy, drug screening, assays for receiver activity, arthritis and inflammation, leukaemias and constructions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed
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                                                                                                                                           Ren F, W.
Zhang J;
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                                                                                                                                        Qian XB,
Yang Y,
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                                                                                                                                      Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 841; 10078pp; English.
                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, us such as central nervous system injuries
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                   2001-442253/47.
                                                                                            (HYSE-) HYSEQ INC
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                                                                                                                                      Tang YT,
Wang J, W
Zhao QA,
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The present invention relates to human kinases (PKIN) and the nucleic acids encoding them. PKIN is used as vaccine and in gene therapy. PKIN is used in the prevention, diagnosis and treatment of diseases cancers, adenocarcinoma, leukemia, sarcoma, immune disorder, Addison's disease, adenocarcinoma, leukemia, sarcoma, immune disorder, Addison's disease, cout, microbial infections, cardiovascular disease and/or inflammation, myasthenia gravis, atherosclerosis, cirrhosis, osteoporosis, myocardial infections, cardiovascular disorder, seizure disorder, infammation, myasthenia gravis, atherosclerosis, cirrhosis, osteoporosis, myocardial infaction, cataract, growth and development disorder, seizure disorder, pulmonary embolism, dauchar's disease, renal disorder, seizure disorder, gissase, prok's disease, renal disorder, seizure disorder associated with decreased PKIN. PKIN may be used to treat disorders associated with decreased PKIN. Complement the patients own production of PKIN, PKIN nucleic assuptonent the patients of production of PKIN, PKIN nucleic acid and the complementary sequences may also be used as DNA probes in nucleic assays to detect and quantitate the presence of similar nucleic acid sequences in samples and therefore which patients may be nucleic acid sequences in samples and therefore which patients may be need of restorative therapy. The present sequence is human PKIN-2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                Yue H, Gandhi AR, Tribouley CM, Kearney L, Griffin JA, Nguyen DB; Bandman O, Lu DAM, Lal P, Burford N, Khan FA, Walia NK, Yao MG; Patterson C, Burrill JD, Marcus GA, Zingler KA, Recipon SA, Lu Y; Policky JL, Thornton M, Tang YT, Hafalia A, Elliott VS, Baughn MK; Walsh RT, Ramkumar J, Borowsky ML, Au-young J, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human kinases and nucleic acids, useful for preventing diagnosing and treating cancers, inflammation and immune disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 GGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATC---AAGAAGTCACC 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 TGCCTTCCGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCATGA 302
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Pred. No. 1.3e-131;
0; Mismatches 275; Indels 6
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                                                        28-APR-2000; 2000US-200226P.
05-MAY-2000; 2000US-202339P.
11-MAY-2000; 2000US-205564P.
26-MAY-2000; 2000US-205564P.
26-MAY-2000; 2000US-207339P.
01-JUN-2000; 2000US-208795P.
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20-APR-2001; 2001WO-US12992
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" Ramkumar J,
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P-PSDB; AAE11768.
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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GCTTGTTTCTGGIGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAGAA 422
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                GGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAGAATGG
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26-JUL-2001

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metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease; reproductive disorder; gene therapy; ss.
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                                                   CATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCTGAAGAGAACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and chromotars.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 AGCTGAAGAGAGAGAGCAACTGCTTTTGCTGTGAAGTGTATCCCTAAGAAGGCGCT 319
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                                                                                                                                                                                                                        Wang
                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGGAAAACCTTCATTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTTTTCCT
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                                                                                                                                                                                                                      Ren F, W
Zhang J;
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                                                                                                                                                                                                                      Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2164 BP; 557 A; 542 C; 560 G; 505 T; 0 other;
                                                                                                                                                                                                                 Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 4413; 10078pp; English
                                                                             19-JUL-2000; 20000S-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653191.
19-CCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                               2000US-0552317.
2000US-0598042.
2000WO-US34263
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                                                                                                                                                                                   (HYSE-) HYSEQ INC
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                             21-JAN-2000;
25-APR-2000;
09-JUL-2000;
 26-DEC-2000;
                                                                                                                                                                                                                 Tang YT,
Wang J, W
Zhao QA,
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                                                                                                                                    Ass06701-AAS06757 encode for novel human protein kinases #1-57. The
novel protein kinases have been identified as members of the tyrosine
or setine/threohine kinase (PTK and STK) familites. The polymouleotides
corstine/threohine kinase (PTK and STK) familites. The polymouleotides
corstine/threohine kinases and the polymoptides may be used in the
provention, diagnosis and treatment of diseases associated with
tages (aspecially cancers of hematopoletic origin), cardiovascular
cancers (aspecially cancers of hematopoletic origin), cardiovascular
disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
immune related diseases (e.g. rheumatorid arthritis), neurological
disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
parkinson's disease), inflammatory disorders (e.g. infertility).
Additionally, polymocleotides encoding protein kinases may be
used for gene therapy and as DNA probes in diagnostic assays.
The protein kinase polypeptides may be used as antigens in the production
of antibodies against the protein kinases and in assays to identify
modulators of protein kinase expression and activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding human kinase polypeptides, useful for prever diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 AAGCAAAGACTGGGAAGCTCTTTGCTCTGAAGTGCATC---AAGAAGTCACCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 ITCCGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCATGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCCTGAAGAGAACTCTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 1074;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 502.2; DB 22; Length
Pred. No. 1.7e-131;
0; Mismatches 273; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1074 BP; 313 A; 258 C; 276 G; 227 T; 0 other;
                                                                                                              Example 1; Figure 1; 433pp; English
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71.3%;
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WPI; 2001-343950/36.
P-PSDB; AAU03508.
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Matches
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TTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGCTCACCACATGAGG 1023
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                                                                                                                        720
                                                                                                                                                                                           GCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCCCCCG
                        TICIATGAAGAAACGGAGICIAAGCITITICGAGAAGAICAAGGAGGGCIACIAIGAGIII
                                                                                                                                                                     GAGTCTCCATTCTGGGATGACATTTCTGAGTCAGCCAAGGACTTTATTTGCCACTTGCTT
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/*tag= a
/transl_except= "(pos: 838..843, aa: Ala)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of a human kinase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Turner CA, Friedrich G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; kinase; human disease; human disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
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Sands AT;
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P-PSDB; AAB84360.
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The present sequence encodes a kinase polypeptide. The kinase polynucleotides and polypeptides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for the detection of mutant kinases, or inappropriately expressed kinases for the diagnosis of a disease or disorder. They are useful for screening for drugs (or high throughput screening of combinatorial libraries) effective in the treatment of symptomatic or phenotypic manifestations of that disease or disorder. The polynucleotide sequence is useful as a source of probes and primers, which can be used to screen libraries, isolate clones, and prepare cloning and sequencing templates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426
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                                                                                                                                                                                                                               Best Local Similarity 71.3
Matches 692; Conservative
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      TTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGCACCACATGAGG 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated human kinase polynucleotide that shares structural similarity with animal kinases including calcium/calmodulin-dependent protein kinases and serine/threonine protein kinases, useful in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of a human kinase polypeptide.
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1..1158
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                             AAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTTTTCCTGGTG 189
GTTTCTGGTGGGGGGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAAGGAT
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                                                 AAGATCTTCGAGTTCAAAGAGACCCTCGGAACCGGGGCCTTTTCCGAAGTGGTTTTAGCT
                                                                     AAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATC---AAGAAGTCACCTGCC
                                                                                                             TTCCGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCATGAAAAC
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Human; death domain-containing receptor; DDCR; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; varucide; fungicide; opthalmological; gene therapy; immunodeficiency disease; Acquired immune deficiency syndrome; AIDS; leukaemia; autoimmune disease; systemic lupus erythematosus; hyperproliferative disorder; neoplasm; cerebrovascular disorder; neroplasm; cerebrovascular disorder; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; ocular disorder; corneal infection; degenerative disease; SWA, apoptosis; spinal muscular atrophy; epithalial cell proliferation; infection; cancer; wound healing; skin aging; chemotaxis; HDPVZ91 clone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNAs and their corresponding proteins. DDCR CDNA and protein are used to prevent, treat or ameliorate a medical condition in mammals. They are also used in diagnosing a pathological condition in mammals. Succeptibility to a pathological condition or susceptibility to a pathological condition. The DDCR protein and its antibodies are used in the diagnosis and treatment of disorders such as immunodeficiency diseases (e.g. Acquired immune deficiency syndrome (AIDS), leukaemia) autoimmune diseases (e.g. Asystemic lupus erythematosus, rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of the breast or liver), cerebrovascular disorders (e.g. cardiac arrest), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), coular disorders (e.g. cardiac arrest), alsease), coular disorders (e.g. corneal infection), degenerative diseases (e.g. spinal muscular atrophy-SMA), infection, abbring tapoptosis, disorders of the placenta or uterus and infection or uterus and infection or uterus and
                                                           domain-containing receptor (DDCR) cDNA from HDPVZ91 clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New death-domain containing receptor polynucleotides and polypeptides, useful for treating and diagnosing cancer \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infections caused by bacteria, viruses and fundi. The DDCR proteins are used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, to support cell culture of primary tissues, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Human death domain-containing receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The patent discloses novel death domain-containing receptor (DDCR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence is human death domain-containing receptor RB) cDNA from clone HDPVZ91 (ATCC No: PTA839).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regenerate tissues and in chemotaxis. The DDCR sequences are in correcting aberrant cellular apoptosis by gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                     04-JUL-2001
                                                               Human death
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Length 1578;

DB 22;

Score 497;

20.3%;

Query Match

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                       GATGACTGCAGTTCCTGGAAGAACAGACCACCAACATCCGGAAAACCTTCATTTTATG 147
         Gaps
                                      15 GAGAGCAGCTCCTCCTGGAAAAAGCAAGCTGAAGACATCAAGAAGATCTTCGAGTTCAAA
                                                     TCCAAGCTCTTTGAGCAGATCCTCAAGGCGGAATATGAGTTTGACTCTCCCTACTGGGAT
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71.68;
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Similarity
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Best Local
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The present sequence is the coding sequence for Murine Dendritic Cell Kinase 3 (MDCK-3). The protein encoded by the present sequence is useful for treating a variety of disorders listed in the disclosure of the specification, including autoimmune disorders, allergic reactions, myeloid or lymphoid cell deficiencies, wound healing and tissue repair and replacement, burns, inclisions and ulcers, periodortal disease, inflammatory diseases, tumours and bacterial, viral or fungal infection. MDCK-3 is a member of the Ca2+/calmodulin-dependent kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                       Novel murine and human kinase nucleic acids useful for treating inflammations, infections, tumors, allergies, autoimmune diseases, and for stimulating or suppressing immune responses
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                                                                          Kinase; MDCK-3; autoimmune disorder; allergy;
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                                                                                         wound healing; periodontal disease; inflammatory disease; infection; Ca2+/calmodulin-dependent kinase family; ss.
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Pred. No. 1.1e-128;
0; Mismatches 279;
                                          Dendritic Cell Kinase 3 coding sequence.
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Les 686; Conserv
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                                                                                                                                       Mus musculus.
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CTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAAG

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                          ACTGCCTGTGGGACCCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAGG 660
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                 ATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCTGAAGAGAACTCT
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BM547443 AGENCORRT B1084897 602869466 B1084101 602869466 B1821474 603038856 B1824483 603038855 B1818261 603032510
SUMMARIES	ID	BM547443 BIO84897 BIO84101 BI821474 BI824483
	DB	133
	Query Sore Match Length DB II	1126 966 1048 809 740
dР	Query Match	39.4 33.8 32.8 32.5 29.5
	Score	963.8 826 801.4 794.2 736.8
	Result No.	Ω . 10 × 4 × 10

BM921532 AGENCOURT BI772626 603060879 BM80735 AGENCOURT BC715920 602676667 B1753035 60302844 B093404 AGENCOURT BC29366 602390829 B1667965 603292877 B183463 603292877 B183463 F03202418 B0102407 ij21c07.x AL34342 DKF2p5470 B0102407 ij21c07.x AL560091 AL560091 AN016039 UI-H-BI0P AN251224 UI-H-BI0P AN251224 UI-H-BI0P AN351224 UI-H-BI0P AN383372 of29311.s	AL556476 AL556476 BQ949629 AGENCOURT BG168668 602319906 AW254051 U1 - R-BJO- B1758466 603022650 AW52224 U1 - R-BOO- BE569540 601328368 BW919261 AGENCOURT AW826802 fk53c02.y AW826802 fk53c02.y AW820558 U1 - R-BJOP BC702279 602683496 AL578723 AL578723 B154545 603187723 AL574819 AL574819 BG895406 358836 MA BQ066920 AGENCOURT B1463145 603207913 B1761267 603044016 BR266955 601191504 BW728439 UI - B-EJO- AJ397261 AJ397261	GNWENTS GNWENTS 6 bp mRNA linear EST 20-FEB-2002 25 Homo sapiens cDNA clone IMAGE:5724450 a; Craniata; Vertebrata; Euteleostomi; s; Catarrhini; Hominidae; Homo. th, Mammalian Gene Collection (MGC) Ph.D. v gen Life Technologies, Inc. Life Technologies, Inc. Life Toomsortium (LLNL) rt Bioscience Corporation one distribution information can be . Consortium/LLNL at: olumn: 19 623.
BM921532 BI775626 BM807335 BG715920 BI753035 BG934044 BG293660 BI667965 BO086330 ALI3434 BO102407 ALS60091 AW016039 AW251224	ALIS56476 BQ46629 BG16868 BQ5229 BG16866 AW522224 BM522224 BW522224 BW522224 BW522224 BW522224 BW526802 BG702279 AL578723 BL578723 BL578245 BL57823 BL578245 BL57823 BL57823 BL57823 BL57823 BL57823 BL57823 BL57823 BL57823	ALIGN 1126 3C_125
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0 00 0	0 0 0	PRES LD DEN BMG PRES SOUTH PRES CON CON CON CONTRACTOR PRES

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/organism="Homo sapiens"
/db.ref="taxon:9606"
/clone_lib="IMAGE:5724450"
/clone_lib="NIELMGE_125"
/clone_lib="NIELMGE_125"
/lab_host="DH10B#
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site_l: EcoRV (destroyed); Site_2: Not!; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size la destroyed upon cloning). Average insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gland for full-length clones and was tracking code 036. "Tobal converse of the converse 
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/clone="Inter-caxon:3000"
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/clone_lib="NIH_MGC_l02"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: salibtory gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRi: cDNA made by oligo-dT priming.
Directionally cloned into EcoRiXAhoI sites using the
following 5' adaptor: GGCAGCAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-DNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 966)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1820 row: d column: 17
High quality sequence stop: 832.
Location/Qualifiers
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                         TTGAGTCTCCATTCTGGGATGACATTTCTGAGTCAGCCAAGGACTTTATTTGCCACTTTG
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: capabs-rémail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                       CTTGAGAAGGATCCGAACGAGCGGTACACCTGT--GAGAAGGCCTTGAGTCATCCC--TG
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    /organism="Homo sapiens"
/db_xref="taxon:9606"

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S ISM CE RS	COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-rémail.nih.gov Tissue Procurement: ArCC CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln.i.gov Plate: LLCM1820 row: d column: 17 High quality sequence stop: 853.	FEATURES Location/Qualifiers 11048 11048	following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." BASE COUNT 231 a 298 c 264 g 254 t 1 others ORIGIN 32 88. COLE 801 4. DE 13. Learth 1048.	Best Local Similarity 93.1%; Pred. No. 8.1e-2015; Lengin 1040; Best Local Similarity 93.1%; Pred. No. 8.1e-2015; Matches 885; Conservative 0; Mismatches 56; Indels 10; Gaps 4; Qy 1425 GGTCATGGTACCAGTTAAAGCCAGTGGCAGCTCCCACTGCCGGGCAGGCA	1405 ANTICOLOGICAL TECCHONOLOGICAL CONTROL OF THE C	182 AGCGCAGGGCTTAGCAGGAGGTTTCTGGCCAGAAGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGC	DD 302 TGTGAGCAGGAGGAGGGTGCCCAGGTTCCAGGTCTCCCTGACCTGCTCTATG 301 Qy 1785 CCCCACACCCTACGTGCCGTGGCTCTGTGCAGGTGTAGGTAG
Matches 913; Conservative 0; Mismatches 30; Indels 9; Ga 1440 TAAAGCCAGTGGCAGTCCCACTGCGGGCAGGCAGACTGGAGTCTGTTCATTATGTG	Unit Unit	1733 GGAGAAGCGGTGCCCACCAGGTTCCAGGTCTCCTGACCTGCTGCTCTATGCCCCACAC 	DD 533 TGTCGTGAAAAGCTTAATGGGCTGGCTGTCACCTTCTCCAAGCAAG	2033 GCTCCCCATGGTGTGTGAGGTCTTCAAGTTCTAACTCTAACTCCAGGATTAG 1111111111111111111111111111111	2153 AAAGCAGTGCCACACCTCCAAGTGGAATAGAAAGAAGTCATGGTAAGGGCTGCAAG 2154 AAAGCAGTGCCACACCTCCAAAGTGGAATAGAAAGAAAGTTCATGAGTAAGGGCTGCAAG 234 AAAGCAGTGCCACCCTCCAAAGGAATAGAAAGAAGTTCATGAGTAAGGGCTGCAAG 2213 GAATTCTTATCCTGGCCACATGTCCTCCGTGCACCCAATGGAGTTAACCTTGGAAG 114 GAATTCTTATCCTGGCCACATGTCCTCCGTGCACCCAATGGAGTTAACCTTGGAAG 1174 GAATTCTTATCCTGGCCACATGGAGTTAACCTTGGAAG	273 TIGACTATITIAATGTCGCAGGAGTTCTAATCCTGCCTGTTCCTTTTCTCTCCTT 114 TIGACTATITIAATGTCTGCCAGGAGTTCTAATCCTGCCTTTCTTTCTCTCCTT 2333 GAAAGTCCAGCAACCATTCTTCTCCCCAGTTTCCTCGCTTTTCTCTCCTT 2341 GAAAGTCCAGCAATCTTGCCTTCCCCAGTTTCTCGCCTCCACC 2384	RESULT 3 B1084101 LOCUS B1084101 LOCUS B1084101 DEFINITION 602869466F1 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:5013856 5', ACCESSION B1084101

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pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
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Homo sapiens cDNA clone IMAGE:5179336 5',
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NIH-WGC http://mgc.nci.nih.gov/.
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National instruction in National (1999) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. clone distribution in National Connection Connection (LINL) found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov http://image.llnl.gov column: 17
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                                        2025 GACAGGCAGCTCCCCATGGTGGTCTGCTGTGAGCTCTTCAAGTTCTAATCGTTAACTCC
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/db_xref="taxon:9606"
/clone="IMAGE:5179336"
/clone_11b="NHH_MGC_115"
/lab_host="DH10B"
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Location/Qualifiers
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      Library is
male lung, age 27; and 1 male testis, age 69. Library 1: oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, Library is normalized and enriched for full-length clones and was constructed by Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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Pred. No. 5.9e-201;
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llarity 99.6%;
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BI824483 740 bp mRNA linear EST 04-OCT-2001 603038855F1 NIH_MGC_115 Homo sapiens CDNA Clone IMAGE:5179957 5',
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 740)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11448 row: m column: 14
High quality sequence stop: 709.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:5179957"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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603032510F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173587 5', mRNA sequence.
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B1818261.1 G1:15928724
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forw-sporgnf6; Site_1: Not!; Site_2: Brook (destroyed): RNA
source anonymous pool of 6 male brains, age range 23-27; I
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (Brook site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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Conteact: Robert Strausberg, Ph.D.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
CLONE distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
CLONE distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://lange.llnl.gov
http://lange.llnl.gov
High quality sequence stop: 742.
Location/Qualifiers
I. 742.
Corganism="Homo Sapiens"
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NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                 541 TCTAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGGCATCATGTCC
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/clone_lib="NIH_MGC_115"
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                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1068)
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                                                                                            GCAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGA 419
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                                                                                                                                                                                                                                                                                                                                                                                                            TCTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAACAGACCAC 119
                                      Gaps
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                                                     1 TGGAGTGGGAGCTCAA-GCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAAC 59
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                                                                                                                                                         CTCTAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGGCATCATGTC
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                                                                                                                                                                                ACCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCA
                                      1;
                       Length 742;
                                      Indels
                       DB 13;
                                      5;
                       Score 720.8; DB 13
Pred. No. 2.4e-181;
                                     0; Mismatches
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197
                       29.5%;
99.6%;
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                                      Matches 733; Conservative
180
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a
197
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Anote—"Organ: pooled brain, lung, testis; Vector:

pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
pcMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
pcMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed);

male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1: 8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: tis is an HLMC Library."
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                                                                                                      Email: cgaps-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation.
CDNA Library Preparation.
CDNA Library Preparation.
CDNA Library Arayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAML2788 row: b column: 19
High quality sequence stop: 592.
Location/Qualifiers
I. 1068
//db_xref="Hemo sapiens"
//db_xref="Hemo sapiens"
//db_xref="Hemo: Sp33010"
//lb_not="NHAGE: 5753010"
//lb_not="INAGE: 5753010"
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   National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAACAGACCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 GGCATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCTGAAGAAACCGAACCACTTACCTTACCCTAGAAGAACACAGAACCCGAAAACCTGAAACCCGGAAAACCTTACCTTACCTTACCCTGAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCAT
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                                                                                    Contact: Robert Strausberg, Ph.D.
NIH-MGC http://mgc.nci.nih.gov/
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240

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BM807335 1129 bp mRNA linear EST 05-MAR-2002
AGENCOURT_6575096 NIH_MGC_124 Homo sapiens CDNA clone IMAGE:5732298
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1129)
                                                                                                                                                                 189 TICCTGGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCA 248
                                                                                                                                                                                                                                                                                                               CCGTICIATGAAGAAACGGAGICTAAGCTITICGAGAAGAICAAGGAGGCTACIAIGAG 780
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                    CCTGCCTTCCGGGACAGCAGCTGGAGAATGAGATTGCTGTGTTTGAAAAAGATCAAGCAT 300
                                                                                                                                                                                                                                        GAAAACATTGTGACCCTGGAGGACATCTATGAGAGCACCACCACTACTACCTGGTCATG 360
                                                                                                                                                                                                                                                                                                                                                                CAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAG 420
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 CTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAACAGACCACC 120
                                                                                                          129 AACATCCGGAAAACCTTCATTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT 188
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                                                                                                                                               TTCCTGGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGAGGTCA
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BM807335
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BM807335
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TITLE
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                                                                                                                                                                                                                                                                                                                                             BI772626 812 bp mRNA linear EST 25-SEP-2001
603060879F1 NIH_MGC_122 Homo sapiens CDNA clone IMAGE:5210299 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: capbar Femail.nih.gov
Email: capbar Femail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1527 row: m column: 20
High quality sequence start: 2
High quality sequence stop: 808.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 812)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) (Uppublished (1999)
                                     613
                                                                                                                                                                 Gaps
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614 ACCTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAG
                                                                         A-CIGCCIGIGGGACCCCAGGCIACGIGGCICCAGAAGIGCIGGCCCAGAAACCCIACAG
                                                                                                                                              660 CAAGGUTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCC
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Pred. No. 2.7e-179;
0; Mismatches 3;
                                                                                                                                                                                                                    720 CCCG-TTCTATGAAGAACGGAGTCTAAGCTTTT 752
                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5210299"
/clone_lib="XHH_MGC_122"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
BI772626
BI772626.1 GI:15764204
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Best Local Similarity 91.0%;
Matches 801; Conservative
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LLNL)
DNA Sequencing by: Inoyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM10688 row: e column: 17
High quality sequence stop: 766.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                661 AAGGC----TGTGGATTGCTGGTCCATCGCCGTCATCA-CCTACATATTGCTCTGTGGATA
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelƙ
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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    . 824
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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BG715920
BG715920.1 GI:13995107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
to column: 19
High quality sequence start: 11
High quality sequence stop: 651.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5732298"
/clone_lib="NIH_MGC_124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="hippocampus"
/lab_host="DH108"
                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 g
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sapiens cDNA clone IMAGE:5196323 5',
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                                                                                                        AACATCCGGAAAACCTTCATTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT 180
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                                                                    CTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAAAAGAACAGACCACC 120
                                                                                                                                                                                                               GAAAACATTGTGACCCTGGAGGACATCTATGAGAGCACCACCACCACTACTACTGGTCATG 360
                                                                                                                                                                                                                                                                                       AAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAGAAT 480
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 731)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                    9
                                                    97
                                          CAGCTIGITICIGGIGGGGAGCTCTITGACCGGATCCTGGAGCGGGGTGTCTACACAGAG
                                                                                                              TTCCTGGTGAAGCAAAGACTGACTGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCA
                                 TGGAGTGGGAGCTCAAGCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAACT
                                                                            CCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAAGATCAAGCAT
                                                                                                                                                                                                                                                            GGCATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCTGAAGAGAAC
                                                                                                                                                                                                                                                                                                                                                                        TCTAAGATCATGATTAGTTTTGGTCTGTCCAAGATGGAACAGAATGGCATCATGTCC
                                                                                                                                                                                                                                                                                                                                                                                                ACTGCCTGTGGGACCCCAGGCTACG-TGGCTCCAGAAGTGCTGGCCCAG-AAACCCTACA
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                  3;
                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCCGTTCTATGAAGAAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4e-176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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      96.98;
      Local Similarity 96.9
nes 747; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
BI753035
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BI753035
LOCUS
DEFINITION
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ORGANISM
       Best Loc
Matches
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AUTHORS
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/urefarism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="Inches:156323"
/clone=lib="NulH_MGC_114"
/lab_host="Dali0B"
//dote="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: ECGRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcGNV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research desectics tracking code 019. Note: this is a NIH_MGC Library.

90 a 182 c 191 g 168 t
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Email: cgapbs-rémail.nih.gov
Tissue procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1491 row: g column: 12
High quality sequence stop: 729.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGAGTGGGAGCTCAAG-CAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAACATCCGGAAAACCTTCATTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGT
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Pred. No. 1.6e-175;
0; Mismatches 0;
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Best Local Similarity 99.7%;
Matches 721; Conservative
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RESULT 13
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                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 905)
NIH-WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:1000"
/db_xref="taxon:1000"
/clone_lb="lwAGE:6336727"
/lab_host="DH10B (phage-resistant)"
/note="Organ: otocysts; Vector: pCMV-SPORT6.1.ccdb;
Site=1: Booky, Site_2: Not!, Cloned unidirectionally.
Primer: Olligo dT. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 653.6; DB 14; Length 905; Pred. No. 2.5e-163; 0; Mismatches 79; Indels 4;
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217 c 240
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90.0%;
                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                         house mouse.
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                                                                                                         720 CCC 722
                                                                                          720 CCC 722
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es 745;
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                                                                                                                                                                                 DEFINITION
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ORIGIN
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BQ934044
LOCUS
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AUTHORS
TITLE
JOURNAL
COMMENT
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BG293660 818 bp mRNA linear EST 21-FEB-2001 602390529F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4502479 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 818)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. i column: 08
High quality sequence stop: 765.

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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Contact: Robert Strausberg, Life Technologies, Inc.
Collection Library Preparation: Life Technologies, Inc.
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AACCTGCTTTACCTTACCCCTGAAGAGAACTCTAAGATCATGATCACTGACTTTGGTCTG
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BG293660
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TITLE
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Mon

Similarity

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107 151 167

47

211

227 271 287 331 347

391

451 467 511

Query Match Local

Matches

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BASE COUNT ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
5 bp mRNA linear EST 12-SEP-2001 sapiens cDNA clone IMAGE:5312346 5',
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Pred. No. 5e-137;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="hypothalamus"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:5312346"
/clone_lib="NIH_MGC_96"
  BI667965
603292877F1 NIH_MGC_96 HOMO
                                               mRNA sequence.
BI667965
BI667965.1 GI:15582198
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ilarity 97.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGTCGGCAGTGAAATACCTACATGAGAATGGCATCGTCCACAGAGACTTAAAGCCCGGAA
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88.0%; Pred. No. 1.7e-146;
ive 0; Mismatches 89;
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RESULT 14 BI667965

630

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527

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purv sportf6; Site_1: Not1; Site_2: ERORV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(ECORV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                         BI834635 554 bp mRNA linear EST 04-OCT-2001 603090418F1 NIH_MGC_120 Homo saplens cDNA clone IMAGE:5229245 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                           GAGNAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAG 477
                                                                                  1 (bases 1 to 554)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs:remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution information on the found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Flate: LLAMIS77 row: c column: 06
High quality sequence stop: 554.
Location/Qualifiers
GCAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCC - - TGGAGCGGGGTGTCTACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.3%; Score 522; DB 13; Length 554; 98.0%; Pred. No. 3.1e-128; Live 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5229245"
/clone_lib="NHH_MGC_120"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                              TGTCCACTGCCTGTGGGACCC 616
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BI834635
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                              262 CTGGAGAATGAGATTGCTGTGTTGAAAAGATCAAGCATGAAAACATTGTGACCCTGGAG
                                                                                                                                   GACATCTATGAGAGCACCACCACTACTACCTGGTCATGCAGCT-----TGTTT
                                                                                                                                                                               GTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAAATGGCATCGTCC
                                                                                                                                                                                                                                                                    491 ACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCTGAAGAGAACTCTAAGATCA
                                                                                                                                                                                                                                                                                                             <u> ACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCACCTGCCTTCCGGGACAGAGGC</u>
                                                                                                                                                                                                              CIGGIGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAGAAGGATGCCA
                                                                                                                                                                                                                                                                                                                                                                                          GGACCCCAGGCTAC 624
                                                                                                                                                                                                                                                                                                                                                                                                      GGACCCCAGGCTAC 554
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Search completed: March 14, 2003, 15:22:05 Job time : 3891 secs